[redacted]

STIC-Biotech/ChemLib 149779

From: Bunner, Bridget
Sent: Monday, April 04, 2005 1:15 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request the following sequence search for case 10/056,583 (please include the pending databases):

(short peptide sequences)

1. the amino acid sequence of SEQ ID NO: 66

2. the amino acid sequence of SEQ ID NO: 96

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up: 4/4/05
Date Completed: 4/5/05
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#: 2
Interference:____ SPDI:___
S/L:_____ Oligomer:____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM: CAOLP
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 16:53:02 ; Search time 117.188 Seconds
(without alignments)
49.505 Million cell updates/sec

Title: US-10-056-583A-66
Perfect score: 71
Sequence: 1 EAKKYEAYKAAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	100.0	15	5	ABP52272	Abp52272 HLA-DR2 m
2	65	91.5	15	5	ABP52270	Abp52270 HLA-DR2 m
3	65	91.5	15	5	ABP52267	Abp52267 HLA-DR2 m
4	60	84.5	15	5	ABP52265	Abp52265 HLA-DR2 m
5	60	84.5	15	5	ABP52271	Abp52271 HLA-DR2 m
6	60	84.5	15	5	ABP52290	Abp52290 HLA-DR2 m
7	60	84.5	15	5	ABP52240	Abp52240 HLA-DR2 m
8	60	84.5	15	5	ABP52292	Abp52292 HLA-DR2 m
9	60	84.5	15	5	ABP52298	Abp52298 HLA-DR2 m
10	60	84.5	17	5	ABP52294	Abp52294 HLA-DR2 m
11	60	84.5	17	5	ABP52296	Abp52296 HLA-DR2 m
12	60	84.5	19	5	ABP52295	Abp52295 HLA-DR2 m
13	59	83.1	15	5	ABP52258	Abp52258 HLA-DR2 m
14	59	83.1	15	5	ABP52257	Abp52257 HLA-DR2 m
15	57	80.3	15	5	ABP52268	Abp52268 HLA-DR2 m
16	56	78.9	15	5	ABP52256	Abp52256 HLA-DR2 m
17	56	78.9	15	5	ABP52241	Abp52241 HLA-DR2 m
18	56	78.9	15	5	ABP52304	Abp52304 HLA-DR2 m
19	56	78.9	15	5	ABP52249	Abp52249 HLA-DR2 m
20	55	77.5	15	5	ABP52261	Abp52261 HLA-DR2 m
21	55	77.5	15	5	ABP52291	Abp52291 HLA-DR2 m
22	55	77.5	15	5	ABP52243	Abp52243 HLA-DR2 m
23	55	77.5	15	5	ABP52269	Abp52269 HLA-DR2 m
24	55	77.5	15	5	ABP52246	Abp52246 HLA-DR2 m
25	55	77.5	15	5	ABP52260	Abp52260 HLA-DR2 m
26	54	76.1	15	5	ABP52237	Abp52237 HLA-DR2 m
27	54	76.1	15	5	ABP52263	Abp52263 HLA-DR2 m
28	53	74.6	15	5	ABP52247	Abp52247 HLA-DR2 m
29	52	73.2	15	5	ABP52255	Abp52255 HLA-DR2 m
30	52	73.2	15	5	ABP52301	Abp52301 HLA-DR2 m
31	52	73.2	15	5	ABP52305	Abp52305 HLA-DR2 m
32	52	73.2	15	5	ABP52266	Abp52266 HLA-DR2 m
33	51	71.8	15	3	AAY58967	Aay58967 Copeptide
34	51	71.8	15	3	AAY82056	Aay82056 MHC class
35	51	71.8	15	4	AAG63191	Aag63191 Peptide w
36	51	71.8	15	5	ABP52251	Abp52251 HLA-DR2 m
37	51	71.8	15	5	ABP52297	Abp52297 HLA-DR2 m
38	51	71.8	15	5	ABP52239	Abp52239 HLA-DR2 m
39	51	71.8	15	5	ABP52274	Abp52274 HLA-DR2 m
40	51	71.8	15	7	ADJ57535	Adj57535 Cop-1 rel
41	51	71.8	15	8	ADQ59594	Adq59594 Copolymer
42	51	71.8	15	8	ADQ81221	Adq81221 Copolymer
43	51	71.8	17	5	ABP52303	Abp52303 HLA-DR2 m
44	50	70.4	15	5	ABP52226	Abp52226 HLA-DR2 m
45	50	70.4	15	5	ABP52227	Abp52227 HLA-DR2 m

ALIGNMENTS

RESULT 1
ABP52272
ID ABP52272 standard; peptide; 15 AA.
XX
AC ABP52272;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:66.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
||||||||||||||||
Db 1 EAKKYEAYKAAAAAA 15

RESULT 2
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
AC ABP52270;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 91.5%; Score 65; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00089;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
|| |||||||||||||
Db 1 EAAKYEAYKAAAAAA 15

RESULT 3
ABP52267
ID ABP52267 standard; peptide; 15 AA.
XX
AC ABP52267;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:61.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 33; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 91.5%; Score 65; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00089;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15

```
                  ||| ||||||||||||
Db          1 EAKAYEAYKAAAAAA 15
```

RESULT 4
ABP52265
ID ABP52265 standard; peptide; 15 AA.
XX
AC ABP52265;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:59.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 33; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

```
  Query Match             84.5%;  Score 60;  DB 5;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 0.0058;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              || ||||||||||||
Db          2 AKAYEAYKAAAAAA 15
```

RESULT 5
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

```
  Query Match             84.5%;  Score 60;  DB 5;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 0.0058;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              |  ||||||||||||
Db          1 EKAKYEAYKAAAAAA 15
```

RESULT 6
ABP52290
ID ABP52290 standard; peptide; 15 AA.
XX
AC ABP52290;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:84.
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 84.5%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
|| |||||||||| |
Db 1 EAPKYEAYKAAAAPA 15

RESULT 7
ABP52240
ID ABP52240 standard; peptide; 15 AA.
XX
AC ABP52240;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:34.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 32; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 84.5%; Score 60; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AKKYEAYKAAAAAA 15
||||||| ||||||
Db 2 AKKYEAYAAAAAAA 15

RESULT 8
ABP52292
ID ABP52292 standard; peptide; 15 AA.
XX
AC ABP52292;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX

PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 84.5%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
|| |||||||||| |
Db 1 EAPKYEAYKAAAAPA 15

RESULT 9
ABP52298
ID ABP52298 standard; peptide; 15 AA.
XX
AC ABP52298;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 84.5%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
| |||||||||||
Db 1 EKAKYEAYKAAAAAA 15

RESULT 10
ABP52294
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 84.5%; Score 60; DB 5; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0066;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
| ||||||||||||
Db 3 EKAKYEAYKAAAAAA 17

RESULT 11
ABP52296
ID ABP52296 standard; peptide; 17 AA.
XX
AC ABP52296;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 84.5%; Score 60; DB 5; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0066;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
| ||||||||||||
Db 1 EKAKYEAYKAAAAAA 15

RESULT 12
ABP52295
ID ABP52295 standard; peptide; 19 AA.
XX
AC ABP52295;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 19 AA;

Query Match 84.5%; Score 60; DB 5; Length 19;
Best Local Similarity 86.7%; Pred. No. 0.0074;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
| ||||||||||||
Db 3 EKAKYEAYKAAAAAA 17

RESULT 13
ABP52258
ID ABP52258 standard; peptide; 15 AA.
XX
AC ABP52258;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:52.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 33; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 83.1%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0083;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
||| | |||||||||
Db 1 EAKAYAAYKAAAAAA 15

RESULT 14
ABP52257
ID ABP52257 standard; peptide; 15 AA.
XX
AC ABP52257;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 32; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 83.1%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0083;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
|| || |||||||||
Db 1 EAAKYAAYKAAAAAA 15

RESULT 15
ABP52268
ID ABP52268 standard; peptide; 15 AA.
XX
AC ABP52268;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:62.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 33; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 80.3%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EAKKYEAYKAAAAAA 15
              ||: |:|||||||||
Db          1 EAEAYKAYKAAAAAA 15
```

Search completed: April 4, 2005, 17:26:03
Job time : 120.188 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:27:14 ; Search time 27.6562 Seconds
(without alignments)
40.488 Million cell updates/sec

Title: US-10-056-583A-66
Perfect score: 71
Sequence: 1 EAKKYEAYKAAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	59.2	391	4	US-09-902-540-11110	Sequence 11110, A
2	41	57.7	731	4	US-09-252-991A-18769	Sequence 18769, A
3	40.5	57.0	109	4	US-09-405-743A-7	Sequence 7, Appli
4	40.5	57.0	109	4	US-09-816-989A-7	Sequence 7, Appli
5	40	56.3	802	4	US-09-489-039A-11230	Sequence 11230, A
6	39	54.9	13	5	PCT-US95-04121-38	Sequence 38, Appl
7	39	54.9	239	4	US-09-248-796A-25676	Sequence 25676, A
8	38	53.5	407	4	US-09-252-991A-29581	Sequence 29581, A
9	38	53.5	419	4	US-09-540-236-3629	Sequence 3629, Ap
10	38	53.5	576	4	US-09-543-681A-7747	Sequence 7747, Ap
11	38	53.5	730	4	US-09-902-540-16253	Sequence 16253, A
12	38	53.5	767	4	US-09-949-016-11664	Sequence 11664, A
13	38	53.5	818	4	US-09-949-016-8579	Sequence 8579, Ap
14	38	53.5	820	4	US-09-949-016-6134	Sequence 6134, Ap
15	37	52.1	13	5	PCT-US94-10257A-33	Sequence 33, Appl
16	37	52.1	105	4	US-09-583-110-4929	Sequence 4929, Ap
17	37	52.1	111	4	US-09-471-276-1532	Sequence 1532, Ap
18	37	52.1	114	4	US-09-107-433-3514	Sequence 3514, Ap
19	37	52.1	118	4	US-09-621-976-4365	Sequence 4365, Ap
20	37	52.1	274	4	US-09-134-000C-3673	Sequence 3673, Ap
21	37	52.1	410	4	US-09-583-110-3852	Sequence 3852, Ap
22	37	52.1	413	3	US-08-669-408B-10	Sequence 10, Appl
23	37	52.1	428	4	US-09-107-433-4072	Sequence 4072, Ap
24	37	52.1	466	4	US-09-489-039A-13950	Sequence 13950, A
25	37	52.1	552	4	US-09-634-238-338	Sequence 338, App
26	37	52.1	629	4	US-10-081-923-6	Sequence 6, Appli
27	37	52.1	664	3	US-08-669-408B-2	Sequence 2, Appli
28	37	52.1	669	4	US-09-878-756-4	Sequence 4, Appli
29	37	52.1	741	4	US-09-949-016-11523	Sequence 11523, A
30	37	52.1	741	4	US-09-949-016-11524	Sequence 11524, A
31	37	52.1	3854	4	US-09-949-016-7876	Sequence 7876, Ap
32	36	50.7	13	5	PCT-US95-04121-60	Sequence 60, Appl
33	36	50.7	54	3	US-09-117-121-30	Sequence 30, Appl
34	36	50.7	56	4	US-09-405-743A-3	Sequence 3, Appli
35	36	50.7	56	4	US-09-816-989A-3	Sequence 3, Appli
36	36	50.7	109	4	US-09-645-593-2	Sequence 2, Appli
37	36	50.7	171	4	US-09-270-767-61141	Sequence 61141, A
38	36	50.7	177	3	US-09-058-562-27	Sequence 27, Appl
39	36	50.7	226	4	US-09-107-532A-4730	Sequence 4730, Ap
40	36	50.7	280	4	US-09-252-991A-23529	Sequence 23529, A
41	36	50.7	301	4	US-09-107-433-4922	Sequence 4922, Ap
42	36	50.7	305	4	US-09-107-433-4018	Sequence 4018, Ap
43	36	50.7	317	4	US-09-248-796A-20634	Sequence 20634, A
44	36	50.7	399	4	US-09-583-110-2754	Sequence 2754, Ap
45	36	50.7	422	4	US-09-252-991A-29504	Sequence 29504, A

ALIGNMENTS

RESULT 1
US-09-902-540-11110
; Sequence 11110, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11110
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11110

Query Match 59.2%; Score 42; DB 4; Length 391;
Best Local Similarity 53.3%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 EAKKYEAYKAAAAAA 15
              :|: | ||||:| :|
Db         81 KAEAYRAYKASAGSA 95
```

RESULT 2
US-09-252-991A-18769
; Sequence 18769, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18769
; LENGTH: 731
; TYPE: PRT

```
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18769

  Query Match             57.7%;  Score 41;  DB 4;  Length 731;
  Best Local Similarity   69.2%;  Pred. No. 87;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KKYEAYKAAAAAA 15
              | ||||:|| | |
Db        177 KIYEAYEAACARA 189


RESULT 3
US-09-405-743A-7
; Sequence 7, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
;  APPLICANT:  Yeda Research and Development Co., Ltd.
;  TITLE OF INVENTION:  GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
;  FILE REFERENCE:  60807-A
;  CURRENT APPLICATION NUMBER: US/09/405,743A
;  CURRENT FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:   SYNTHETIC
;   OTHER INFORMATION: PEPTIDE
US-09-405-743A-7

  Query Match             57.0%;  Score 40.5;  DB 4;  Length 109;
  Best Local Similarity   66.7%;  Pred. No. 15;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 EAKKYE---AYKAAAAAA 15
              |||| |   |||| || |
Db         83 EAKKAEAAKAYKAEAAKA 100


RESULT 4
US-09-816-989A-7
; Sequence 7, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
;  APPLICANT: Gad, Alexander
;  APPLICANT:  Lis, Doris
;  TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
;  TITLE OF INVENTION:  AND FOR THERAPEUTIC USE
;  FILE REFERENCE: 2609/60807-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/816,989A
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: 60/101,693
;  PRIOR FILING DATE: 1998-09-25
;  PRIOR APPLICATION NUMBER: PCT/US99/22402
;  PRIOR FILING DATE: 1999-09-24
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-7

  Query Match             57.0%;  Score 40.5;  DB 4;  Length 109;
  Best Local Similarity   66.7%;  Pred. No. 15;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 EAKKYE---AYKAAAAAA 15
              |||| |   |||| || |
Db         83 EAKKAEAAKAYKAEAAKA 100


RESULT 5
US-09-489-039A-11230
; Sequence 11230, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 11230
;   LENGTH: 802
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11230

  Query Match             56.3%;  Score 40;  DB 4;  Length 802;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches   10;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              | |: ||  ||||||
Db        375 ERKRQEAEAAAAAAA 389


RESULT 6
PCT-US95-04121-38
; Sequence 38, Application PC/TUS9504121
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Haptenated Peptides and Uses Thereof
;    NUMBER OF SEQUENCES:  62
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/222,206
;      FILING DATE:  April 1, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vanstone, Darlene A.
;      REGISTRATION NUMBER:  35,279
;      REFERENCE/DOCKET NUMBER:  079.2PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 466-6000
;      TELEFAX:  (617) 466-6010
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
PCT-US95-04121-38

  Query Match             54.9%;  Score 39;  DB 5;  Length 13;
  Best Local Similarity   81.8%;  Pred. No. 3;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          5 YEAYKAAAAAA 15
              |:| |||||||
Db          3 YKAAKAAAAAA 13


RESULT 7
US-09-248-796A-25676
; Sequence 25676, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25676
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-25676

  Query Match             54.9%;  Score 39;  DB 4;  Length 239;
  Best Local Similarity   71.4%;  Pred. No. 58;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAA 14
              |||| || | | ||
Db        131 EAKKAEAAKKAEAA 144


RESULT 8
US-09-252-991A-29581
; Sequence 29581, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 29581
;   LENGTH: 407
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581

  Query Match             53.5%;  Score 38;  DB 4;  Length 407;
  Best Local Similarity   69.2%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAA 13
              ||:| || ||| |
Db        179 EARKAEAQKAAEA 191


RESULT 9
US-09-540-236-3629
; Sequence 3629, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2005-001
;  CURRENT APPLICATION NUMBER: US/09/540,236
;  CURRENT FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3629
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: M.catarrhalis
US-09-540-236-3629

  Query Match             53.5%;  Score 38;  DB 4;  Length 419;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              | || ||:| | | |
Db        136 EWKKREAPKKAGATA 150


RESULT 10
US-09-543-681A-7747
; Sequence 7747, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7747
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-7747

  Query Match             53.5%;  Score 38;  DB 4;  Length 576;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAA 14
              | ::::|||| | |
Db        311 EEEQFQAYKAVAEA 324


RESULT 11
US-09-902-540-16253
; Sequence 16253, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16253
;   LENGTH: 730
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-16253

  Query Match             53.5%;  Score 38;  DB 4;  Length 730;
```

```
  Best Local Similarity   57.1%;  Pred. No. 2.6e+02;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              |: |:| :|| |||
Db        690 AQDYDALRAAGAAA 703


RESULT 12
US-09-949-016-11664
; Sequence 11664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11664
;   LENGTH: 767
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11664

  Query Match             53.5%;  Score 38;  DB 4;  Length 767;
  Best Local Similarity   64.3%;  Pred. No. 2.8e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAA 14
              |||: |   |||||
Db        257 EAKRREVLSAAAAA 270


RESULT 13
US-09-949-016-8579
; Sequence 8579, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8579
;   LENGTH: 818
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8579

  Query Match             53.5%;  Score 38;  DB 4;  Length 818;
  Best Local Similarity   64.3%;  Pred. No. 3e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAA 14
              |||| |   ||:||
Db        307 EAKKREVLSAASAA 320


RESULT 14
US-09-949-016-6134
; Sequence 6134, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6134
;   LENGTH: 820
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6134

  Query Match             53.5%;  Score 38;  DB 4;  Length 820;
  Best Local Similarity   64.3%;  Pred. No. 3e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAA 14
              |||| |   ||:||
Db        307 EAKKREVLSAASAA 320


RESULT 15
PCT-US94-10257A-33
; Sequence 33, Application PC/TUS9410257A
;  GENERAL INFORMATION:
;    APPLICANT:  IMMULOGIC PHARMACEUTICAL CORPORATION
;    APPLICANT:  BRIGITTE DEVAUX
;    APPLICANT:  JONATHAN B. ROTHBARD
;    APPLICANT:  DAWN SMILEK
;    TITLE OF INVENTION:  USES OF MYELIN OLIGODENDROCYTE
;    TITLE OF INVENTION:  GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
;    TITLE OF INVENTION:  RELATED TO AUTOIMMUNE DISEASE
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMULOGIC PHARMACEUTICAL CORPORATION
;      STREET:  610 LINCOLN STREET
;      CITY:  WALTHAM
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02145
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10257A
;      FILING DATE:  1 SEPTEMBER 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/116,824
;      FILING DATE:  03-SEP-1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ANNE I CRAIG
;      REGISTRATION NUMBER:  32,976
;      REFERENCE/DOCKET NUMBER:  071.1 PCT
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-10257A-33

Query Match 52.1%; Score 37; DB 5; Length 13;
Best Local Similarity 81.8%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 YEAYKAAAAAA 15
              | | |||||||
Db          3 YAAAKAAAAAA 13
```

Search completed: April 4, 2005, 17:47:39
Job time : 28.6562 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:21:54 ; Search time 88.5938 Seconds
(without alignments)
56.143 Million cell updates/sec

Title: US-10-056-583A-66
Perfect score: 71
Sequence: 1 EAKKYEAYKAAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	100.0	15	14	US-10-056-583-66	Sequence 66, Appl
2	65	91.5	15	14	US-10-056-583-61	Sequence 61, Appl
3	65	91.5	15	14	US-10-056-583-64	Sequence 64, Appl
4	60	84.5	15	14	US-10-056-583-34	Sequence 34, Appl
5	60	84.5	15	14	US-10-056-583-59	Sequence 59, Appl
6	60	84.5	15	14	US-10-056-583-65	Sequence 65, Appl
7	60	84.5	15	14	US-10-056-583-84	Sequence 84, Appl
8	60	84.5	15	14	US-10-056-583-86	Sequence 86, Appl
9	60	84.5	17	14	US-10-056-583-88	Sequence 88, Appl
10	60	84.5	17	14	US-10-056-583-90	Sequence 90, Appl
11	60	84.5	19	14	US-10-056-583-89	Sequence 89, Appl
12	59	83.1	15	14	US-10-056-583-51	Sequence 51, Appl
13	59	83.1	15	14	US-10-056-583-52	Sequence 52, Appl
14	57	80.3	15	14	US-10-056-583-62	Sequence 62, Appl
15	56	78.9	15	14	US-10-056-583-35	Sequence 35, Appl
16	56	78.9	15	14	US-10-056-583-43	Sequence 43, Appl
17	56	78.9	15	14	US-10-056-583-50	Sequence 50, Appl
18	56	78.9	15	14	US-10-056-583-98	Sequence 98, Appl
19	55	77.5	15	14	US-10-056-583-37	Sequence 37, Appl
20	55	77.5	15	14	US-10-056-583-40	Sequence 40, Appl
21	55	77.5	15	14	US-10-056-583-54	Sequence 54, Appl
22	55	77.5	15	14	US-10-056-583-55	Sequence 55, Appl
23	55	77.5	15	14	US-10-056-583-63	Sequence 63, Appl
24	55	77.5	15	14	US-10-056-583-85	Sequence 85, Appl
25	54	76.1	15	14	US-10-056-583-31	Sequence 31, Appl
26	54	76.1	15	14	US-10-056-583-57	Sequence 57, Appl
27	53	74.6	15	14	US-10-056-583-41	Sequence 41, Appl
28	52	73.2	15	14	US-10-056-583-49	Sequence 49, Appl
29	52	73.2	15	14	US-10-056-583-60	Sequence 60, Appl
30	52	73.2	15	14	US-10-056-583-95	Sequence 95, Appl
31	52	73.2	15	14	US-10-056-583-99	Sequence 99, Appl
32	51	71.8	15	9	US-09-765-301-17	Sequence 17, Appl
33	51	71.8	15	10	US-09-765-644A-17	Sequence 17, Appl
34	51	71.8	15	14	US-10-056-583-33	Sequence 33, Appl
35	51	71.8	15	14	US-10-056-583-45	Sequence 45, Appl
36	51	71.8	15	14	US-10-056-583-68	Sequence 68, Appl
37	51	71.8	15	14	US-10-056-583-91	Sequence 91, Appl
38	51	71.8	15	14	US-10-056-583-92	Sequence 92, Appl
39	51	71.8	15	15	US-10-438-538-21	Sequence 21, Appl
40	51	71.8	17	14	US-10-056-583-97	Sequence 97, Appl
41	50	70.4	15	14	US-10-056-583-20	Sequence 20, Appl
42	50	70.4	15	14	US-10-056-583-21	Sequence 21, Appl
43	50	70.4	15	14	US-10-056-583-24	Sequence 24, Appl
44	50	70.4	15	14	US-10-056-583-42	Sequence 42, Appl
45	50	70.4	15	14	US-10-056-583-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

Query Match 100.0%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
||||||||||||||||
Db 1 EAKKYEAYKAAAAAA 15

RESULT 2
US-10-056-583-61

```
; Sequence 61, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-61

  Query Match             91.5%;  Score 65;  DB 14;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 0.00061;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              ||| ||||||||||
Db          1 EAKAYEAYKAAAAAA 15


RESULT 3
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

  Query Match             91.5%;  Score 65;  DB 14;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 0.00061;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              || ||||||||||||
Db          1 EAAKYEAYKAAAAAA 15


RESULT 4
US-10-056-583-34
; Sequence 34, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-34

  Query Match             84.5%;  Score 60;  DB 14;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 0.004;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              ||||||| ||||||
Db          2 AKKYEAYAAAAAAA 15


RESULT 5
US-10-056-583-59
; Sequence 59, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-59

  Query Match             84.5%;  Score 60;  DB 14;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 0.004;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              || ||||||||||||
Db          2 AKAYEAYKAAAAAA 15


RESULT 6
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
```

```
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

  Query Match             84.5%;  Score 60;  DB 14;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 0.004;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              |  ||||||||||||
Db          1 EKAKYEAYKAAAAAA 15


RESULT 7
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

  Query Match             84.5%;  Score 60;  DB 14;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 0.004;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              || ||||||||||| |
Db          1 EAPKYEAYKAAAAPA 15


RESULT 8
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

  Query Match             84.5%;  Score 60;  DB 14;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 0.004;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              || ||||||||||| |
Db          1 EAPKYEAYKAAAAPA 15


RESULT 9
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

  Query Match             84.5%;  Score 60;  DB 14;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 0.0045;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              |  ||||||||||||
Db          3 EKAKYEAYKAAAAAA 17


RESULT 10
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

Query Match 84.5%; Score 60; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0045;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
| ||||||||||||
Db 1 EKAKYEAYKAAAAAA 15

RESULT 11
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89

Query Match 84.5%; Score 60; DB 14; Length 19;
Best Local Similarity 86.7%; Pred. No. 0.0051;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
| ||||||||||||
Db 3 EKAKYEAYKAAAAAA 17

RESULT 12
US-10-056-583-51
; Sequence 51, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51

Query Match 83.1%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
|| || |||||||||
Db 1 EAAKYAAYKAAAAAA 15

RESULT 13
US-10-056-583-52
; Sequence 52, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-52

Query Match 83.1%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
||| | |||||||||
Db 1 EAKAYAAYKAAAAAA 15

RESULT 14
US-10-056-583-62
; Sequence 62, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-62

Query Match 80.3%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.012;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
||: |:|||||||||
Db 1 EAEAYKAYKAAAAAA 15

```
RESULT 15
US-10-056-583-35
; Sequence 35, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-35

  Query Match             78.9%;  Score 56;  DB 14;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 0.018;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              |:||||| ||||||
Db          2 AEKYEAYAAAAAAA 15


Search completed: April  4, 2005, 17:34:52
Job time : 88.5938 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:01:24 ; Search time 24.8438 Seconds
(without alignments)
58.093 Million cell updates/sec

Title: US-10-056-583A-66
Perfect score: 71
Sequence: 1 EAKKYEAYKAAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	59.2	188	2	I50145	homeotic protein H
2	42	59.2	289	2	A43562	homeotic protein H
3	42	59.2	950	2	T22592	hypothetical prote
4	41	57.7	254	2	H86355	probable 14-3-3 pr
5	41	57.7	728	2	H82965	DNA helicase II PA
6	40	56.3	189	2	S77930	exoskeletal protei
7	40	56.3	189	2	S77935	exoskeletal protei
8	40	56.3	1857	1	S01787	fatty-acid synthas
9	39	54.9	40	2	S58853	homeotic protein u
10	39	54.9	124	2	E84764	hypothetical prote
11	39	54.9	165	2	B87702	ribosomal protein
12	39	54.9	389	2	D26995	homeotic protein U
13	39	54.9	458	2	B87335	hypothetical prote
14	38	53.5	244	2	S40436	histone H1 - midge
15	38	53.5	261	2	T51222	hypothetical prote
16	38	53.5	265	2	S19113	cgcr-4 protein - C
17	38	53.5	346	2	C82156	conserved hypothet
18	38	53.5	347	2	E83525	TolA protein PA097
19	38	53.5	428	2	E87463	hypothetical prote
20	38	53.5	513	2	G96757	probable protein A
21	38	53.5	575	2	AC0364	phosphoenolpyruvat
22	38	53.5	594	2	G70545	hypothetical glyci
23	38	53.5	735	2	T49622	hypothetical prote
24	38	53.5	760	2	I58159	protein kinase C-r
25	38	53.5	760	2	S55473	chloride channel 3
26	38	53.5	820	2	I37240	chloride channel p
27	38	53.5	1239	1	QQBE10	BOLF1 protein - hu
28	37	52.1	170	2	G81426	H+-transporting tw
29	37	52.1	201	2	A81120	conserved hypothet
30	37	52.1	292	2	T40637	40s ribosomal prot
31	37	52.1	339	2	S39979	chitinase (EC 3.2.
32	37	52.1	340	2	S40414	chitinase (EC 3.2.
33	37	52.1	361	2	T12470	hypothetical prote
34	37	52.1	373	2	A69773	hypothetical prote
35	37	52.1	384	2	D81007	GTP-binding protei
36	37	52.1	413	2	S55890	plasma protein rec
37	37	52.1	420	2	B75333	twitching mobility
38	37	52.1	490	2	I41024	colicin 10 - Esche
39	37	52.1	525	2	A45053	proteinase RPI - R
40	37	52.1	527	2	E69351	phosphoglycerate d
41	37	52.1	537	2	AF2785	lipoprotein [impor
42	37	52.1	562	2	H97564	43K antigen (AF157
43	37	52.1	573	2	H82257	phosphoenolpyruvat
44	37	52.1	577	2	F98004	phosphoenolpyruvat
45	37	52.1	577	2	D95136	phosphoenolpyruvat

ALIGNMENTS

RESULT 1
I50145
homeotic protein Hox M - chicken
N;Alternate names: CHOX M
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: I50145; S14512
R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A;Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vir
A;Reference number: I50145; MUID:91238215; PMID:1674560
A;Accession: I50145
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-188 <CRO>
A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g6270
C;Genetics:
A;Gene: CHOX M
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;96-152/Domain: homeobox homology <HOX>

Query Match 59.2%; Score 42; DB 2; Length 188;
Best Local Similarity 81.8%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 YEAYKAAAAAA 15
| |||||||
Db 10 YSKYKAAAAAA 20

RESULT 2
A43562
homeotic protein Hox D8 - mouse
N;Alternate names: homeotic protein Hox 4.3
C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubo
Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob
A;Reference number: A43562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-289 <IZP>
A;Cross-references: UNIPROT:P23463
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>

Query Match 59.2%; Score 42; DB 2; Length 289;

```
  Best Local Similarity   81.8%;  Pred. No. 16;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 YEAYKAAAAAA 15
              |  ||||||||
Db         10 YSKYKAAAAAA 20


RESULT 3
T22592
hypothetical protein F53H10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22592
R;Wilkinson, J.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19586
A;Accession: T22592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-950 <WIL>
A;Cross-references: UNIPROT:Q20733; EMBL:Z77664; PIDN:CAB01216.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F53H10
C;Genetics:
A;Gene: CESP:F53H10.2
A;Map position: 5
A;Introns: 89/3; 124/3; 151/3; 201/3; 236/3; 267/2; 293/3; 340/2; 393/3; 501/2; 550/1; 6

  Query Match             59.2%;  Score 42;  DB 2;  Length 950;
  Best Local Similarity   66.7%;  Pred. No. 48;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              ||| ::|  ||||||
Db        817 EAKAHDAQVAAAAAA 831


RESULT 4
H86355
probable 14-3-3 protein T16E15.8 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86355
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <STO>
A;Cross-references: UNIPROT:P48347; GB:AE005172; NID:g9392684; PIDN:AAF87261.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: 14-3-3 protein

  Query Match             57.7%;  Score 41;  DB 2;  Length 254;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 EAYKAAAAAA 15
              |||||| |||
Db        151 EAYKAAVAAA 160


RESULT 5
H82965
DNA helicase II PA5443 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H82965
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H82965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-728 <STO>
A;Cross-references: UNIPROT:Q9L7T3; GB:AE004957; GB:AE004091; NID:g9951770; PIDN:AAG088?
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: uvrD; PA5443
C;Superfamily: helicase II

  Query Match             57.7%;  Score 41;  DB 2;  Length 728;
  Best Local Similarity   69.2%;  Pred. No. 55;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KKYEAYKAAAAAA 15
              | ||||:|| | |
Db        174 KIYEAYEAACARA 186


RESULT 6
S77930
exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homa
A;Reference number: S77925
A;Accession: S77930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M496

  Query Match             56.3%;  Score 40;  DB 2;  Length 189;
  Best Local Similarity   53.3%;  Pred. No. 22;
  Matches    8;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              :|: ::|:||| |||
Db         12 KARFFQAFKAAEAAA 26


RESULT 7
S77935
exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77935
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homa
A;Reference number: S77925
A;Accession: S77935
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M495

  Query Match             56.3%;  Score 40;  DB 2;  Length 189;
  Best Local Similarity   53.3%;  Pred. No. 22;
```

```
  Matches    8;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              :|: ::|:||| |||
Db         12 KARFFQAFKAAEAAA 26


RESULT 8
S01787
fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum
N;Alternate names: fatty acid synthetase
C;Species: Penicillium griseofulvum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S01787
R;Wiesner, P.; Beck, J.; Beck, K.F.; Ripka, S.; Mueller, G.; Luecke, S.; Schweizer, E.
Eur. J. Biochem. 177, 69-79, 1988
A;Title: Isolation and sequence analysis of the fatty acid synthetase FAS2 gene from Per
A;Reference number: S01787; MUID:89030697; PMID:3053172
A;Accession: S01787
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1857 <WIE>
A;Cross-references: UNIPROT:P15368; GB:M37461; NID:g169179; PIDN:AAA33695.1; PID:g169180
A;Note: the source is designated as Penicillium patulum
C;Genetics:
A;Gene: fas2
C;Superfamily: yeast fatty-acid synthase
C;Keywords: acyltransferase; coenzyme A

  Query Match             56.3%;  Score 40;  DB 1;  Length 1857;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAA 13
              | ||||| || :
Db         62 ASKYEAYDAATS 73


RESULT 9
S58853
homeotic protein ultrabithorax homolog - Junonia coenia (fragment)
N;Alternate names: ultrabithorax homeodomain protein
C;Species: Junonia coenia
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 16-Aug-2004
C;Accession: S58853
R;Warren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
A;Title: Evolution of homeotic gene regulation and function in flies and butterflies.
A;Reference number: S58850; MUID:95075456; PMID:7840822
A;Accession: S58853
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-40 <WAR>
A;Cross-references: UNIPROT:Q25210; EMBL:L42137
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

  Query Match             54.9%;  Score 39;  DB 2;  Length 40;
  Best Local Similarity   60.0%;  Pred. No. 7.4;
  Matches    9;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              : |: :| |||||||
Db         14 QEKQAQAQKAAAAAA 28


RESULT 10
E84764
hypothetical protein At2g35090 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84764
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <STO>
A;Cross-references: UNIPROT:O82182; GB:AE002093; NID:g3668094; PIDN:AAC61826.1; GSPDB:G
C;Genetics:
A;Gene: At2g35090
A;Map position: 2

  Query Match             54.9%;  Score 39;  DB 2;  Length 124;
  Best Local Similarity   60.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              || || ||   | ||
Db         99 EAVKYAAYTLVAVAA 113


RESULT 11
B87702
ribosomal protein S16 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87702
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87702
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <STO>
A;Cross-references: UNIPROT:P58122; GB:AE005673; NID:g13425408; PIDN:AAK25614.1; GSPDB:
C;Genetics:
A;Gene: CC3652

  Query Match             54.9%;  Score 39;  DB 2;  Length 165;
  Best Local Similarity   66.7%;  Pred. No. 29;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              ||:|  | :||||||
Db        125 EAEKAAAAEAAAAAA 139


RESULT 12
D26995
homeotic protein Ultrabithorax, splice form Ib - fruit fly (Drosophila melanogaster)
N;Contains: homeotic protein Ultrabithorax, splice form Ia; homeotic protein Ultrabitho
rm IVa; homeotic protein Ultrabithorax, splice form IVb
C;Species: Drosophila melanogaster
C;Date: 16-Jun-1988 #sequence_revision 16-Jun-1988 #text_change 16-Aug-2004
C;Accession: D26995; B26995; C26995; A30173; B30173; C30173; D30173; E30173; F30173; A0
R;Weinzierl, R.; Axton, J.M.; Ghysen, A.; Akam, M.
Genes Dev. 1, 386-397, 1987
A;Title: Ultrabithorax mutations in constant and variable regions of the protein coding
A;Reference number: A26995
A;Accession: D26995
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <WEI1>
A;Cross-references: UNIPROT:P83949
A;Accession: B26995
A;Molecule type: DNA
A;Residues: 274-287 <WEI2>
```

A;Cross-references: EMBL:X05725; EMBL:Y00206
A;Accession: C26995
A;Molecule type: DNA
A;Residues: 340-361 <WEI>
A;Cross-references: EMBL:X05727; EMBL:Y00206
R;Kornfeld, K.; Saint, R.B.; Beachy, P.A.; Harte, P.J.; Peattie, D.A.; Hogness, D.S.
Genes Dev. 3, 243-258, 1989
A;Title: Structure and expression of a family of Ultrabithorax mRNAs generated by altern
A;Reference number: A30173; MUID:89232720; PMID:2565858
A;Accession: A30173
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-389 <KOR1>
A;Cross-references: GB:X76210; NID:g433476; PIDN:CAA53803.1; PID:g433477
A;Experimental source: splice form Ib
A;Accession: B30173
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-247,257-389 <KOR2>
A;Cross-references: GB:X76210; NID:g433476
A;Experimental source: splice form Ia
A;Accession: C30173
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-257,275-389 <KOR3>
A;Cross-references: GB:X76210; NID:g433476
A;Experimental source: splice form IIb
A;Accession: D30173
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-247,274-389 <KOR4>
A;Cross-references: GB:X76210; NID:g433476
A;Experimental source: splice form IIa
A;Accession: E30173
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-256,291-389 <KOR5>
A;Cross-references: GB:X76210; NID:g433476
A;Experimental source: splice form IVb
A;Accession: F30173
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-247,291-389 <KOR6>
A;Cross-references: GB:X76210; NID:g433476
A;Experimental source: splice form IVa
R;McGinnis, W.; Garber, R.L.; Wirz, J.; Kuroiwa, A.; Gehring, W.J.
Cell 37, 403-408, 1984
A;Title: A homologous protein-coding sequence in Drosophila homeotic genes and its conse
A;Reference number: A90847; MUID:84205674; PMID:6327065
A;Accession: A03319
A;Molecule type: DNA
A;Residues: 'ST',290-329,'Y',331-339,'E',341-361 <MCG>
A;Cross-references: GB:K01959; NID:g157631; PIDN:AAA28615.1; PID:g157632
C;Comment: This homeotic protein controls development of cells in the posterior thoracic
C;Genetics:
A;Gene: FlyBase:Ubx
A;Cross-references: FlyBase:FBgn0003944
A;Map position: 3R,58.8 (89E1,2)
C;Superfamily: homeobox homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;296-352/Domain: homeobox homology <HOX>

  Query Match 54.9%; Score 39; DB 2; Length 389;
  Best Local Similarity 60.0%; Pred. No. 65;
  Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
: |: :| |||||||
Db 363 QEKQAQAQKAAAAAA 377

RESULT 13
B87335
hypothetical protein CC0693 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87335
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87335
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: UNIPROT:Q9AAB1; GB:AE005673; NID:g13421914; PIDN:AAK22678.1; GSPDB:(
C;Genetics:
A;Gene: CC0693

  Query Match 54.9%; Score 39; DB 2; Length 458;
  Best Local Similarity 66.7%; Pred. No. 76;
  Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EAKKYEAYKAAAAAA 15
||| | | || || |
Db 168 EAKVYAAEKAKAAEA 182

RESULT 14
S40436
histone H1 - midge (Chironomus thummi thummi)
C;Species: Chironomus thummi thummi
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40436; S32656
R;Hankeln, T.; Schmidt, E.R.
J. Mol. Biol. 234, 1301-1307, 1993
A;Title: Divergent evolution of an "orphon" histone gene cluster in Chironomus.
A;Reference number: S40435; MUID:94087747; PMID:8263935
A;Accession: S40436
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-244 <HAN>
A;Cross-references: UNIPROT:Q07134; EMBL:X72803; NID:g297559; PIDN:CAA51322.1; PID:g297
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Superfamily: histone H1

  Query Match 53.5%; Score 38; DB 2; Length 244;
  Best Local Similarity 71.4%; Pred. No. 61;
  Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AKKYEAYKAAAAAA 15
||| || || |||
Db 205 AKKPEAKKATKAAA 218

RESULT 15
T51222
hypothetical protein B24M22.180 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C;Accession: T51222
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25286
A;Accession: T51222
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <SCH>
A;Cross-references: UNIPROT:Q9P390; EMBL:AL390354; GSPDB:GN00116; NCSP:B24M22.180
A;Experimental source: strain OR74A
C;Genetics:
A;Gene: NCSP:B24M22.180
A;Map position: 6
A;Introns: 250/1

Query Match 53.5%; Score 38; DB 2; Length 261;
Best Local Similarity 71.4%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 AKKYEAYKAAAAAA 15
              | | |  |||||||
Db        116 APKQEQSKAAAAAA 129
```

Search completed: April 4, 2005, 17:27:05
Job time : 29.8438 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:02:08 ; Search time 111.094 Seconds
(without alignments)
69.141 Million cell updates/sec

Title: US-10-056-583A-66
Perfect score: 71
Sequence: 1 EAKKYEAYKAAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	66.2	840	2	Q6MBW7	Q6mbw7 parachlamyd
2	46	64.8	1038	2	Q8MQW9	Q8mqw9 drosophila
3	46	64.8	2347	2	Q8INH9	Q8inh9 drosophila
4	46	64.8	2451	2	Q9VG05	Q9vg05 drosophila
5	45	63.4	847	2	Q6M9S8	Q6m9s8 parachlamyd
6	45	63.4	867	2	Q6MBH0	Q6mbh0 parachlamyd
7	44	62.0	380	2	Q8W0D1	Q8w0d1 oryza sativ
8	44	62.0	390	2	Q6I5H3	Q6i5h3 oryza sativ
9	44	62.0	853	2	Q7S637	Q7s637 neurospora
10	42	59.2	188	1	HXD8_CHICK	P23459 gallus gall
11	42	59.2	235	2	Q8S703	Q8s703 oryza sativ
12	42	59.2	289	1	HXD8_MOUSE	P23463 mus musculu
13	42	59.2	289	2	Q8IXZ1	Q8ixz1 homo sapien
14	42	59.2	290	1	HXD8_HUMAN	P13378 homo sapien
15	42	59.2	364	2	Q6AY89	Q6ay89 rattus norv
16	42	59.2	391	2	Q8KRC9	Q8krc9 myxococcus
17	42	59.2	900	2	Q20733	Q20733 caenorhabdi
18	41	57.7	131	2	Q89D24	Q89d24 bradyrhizob
19	41	57.7	183	2	Q8RZ94	Q8rz94 oryza sativ
20	41	57.7	254	1	143A_ARATH	P48347 arabidopsis
21	41	57.7	319	2	Q8T762	Q8t762 branchiosto
22	41	57.7	361	2	Q8C7Q4	Q8c7q4 mus musculu
23	41	57.7	728	2	Q9L7T3	Q9l7t3 pseudomonas
24	41	57.7	847	2	Q7SC23	Q7sc23 neurospora
25	40	56.3	189	2	Q7M495	Q7m495 homarus ame
26	40	56.3	189	2	Q7M496	Q7m496 homarus ame
27	40	56.3	232	2	Q6WCQ7	Q6wcq7 ixodes scap
28	40	56.3	237	2	Q6C1J7	Q6c1j7 yarrowia li
29	40	56.3	466	2	Q64Z47	Q64z47 bacteroides
30	40	56.3	512	2	Q7XVB8	Q7xvb8 oryza sativ
31	40	56.3	575	2	Q7WWX1	Q7wwx1 alcaligenes
32	40	56.3	603	2	Q64JV8	Q64jv8 plasmodium
33	40	56.3	608	2	Q64JV9	Q64jv9 plasmodium
34	40	56.3	608	2	Q64JW1	Q64jw1 plasmodium
35	40	56.3	614	2	Q64JV2	Q64jv2 plasmodium
36	40	56.3	727	2	Q64JU8	Q64ju8 plasmodium
37	40	56.3	727	2	Q64JV3	Q64jv3 plasmodium
38	40	56.3	727	2	Q64JV7	Q64jv7 plasmodium
39	40	56.3	746	2	Q9W4M9	Q9w4m9 drosophila
40	40	56.3	747	2	Q7PIN7	Q7pin7 anopheles g
41	40	56.3	751	2	O97427	O97427 drosophila
42	40	56.3	765	2	Q9XBT6	Q9xbt6 klebsiella
43	40	56.3	785	2	Q869D8	Q869d8 ascidia syd
44	40	56.3	810	2	Q64JV4	Q64jv4 plasmodium
45	40	56.3	822	2	Q8IQN2	Q8iqn2 drosophila

ALIGNMENTS

RESULT 1
Q6MBW7
ID Q6MBW7 PRELIMINARY; PRT; 840 AA.
AC Q6MBW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=pc1208;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA Rattei T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX908798; CAF23932.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 840 AA; 96146 MW; 1F1542949F953C4D CRC64;

Query Match 66.2%; Score 47; DB 2; Length 840;
Best Local Similarity 81.8%; Pred. No. 49;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EAKKYEAYKAA 11
              |||:|||||  |
Db        712 EAKRYEAYKIA 722
```

RESULT 2
Q8MQW9
ID Q8MQW9 PRELIMINARY; PRT; 1038 AA.
AC Q8MQW9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SD05989p (Fragment).
GN ORFNames=CG7518;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

```
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY122252; AAM52764.1; -.
DR   FlyBase; FBgn0038108; CG7518.
FT   NON_TER       1      1
SQ   SEQUENCE   1038 AA;  109059 MW;  80C935A2C6D8A276 CRC64;

  Query Match             64.8%;  Score 46;  DB 2;  Length 1038;
  Best Local Similarity   73.3%;  Pred. No. 86;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              :||| || :||||||
Db        101 KAKKKEAKRAAAAAA 115


RESULT 3
Q8INH9
ID   Q8INH9      PRELIMINARY;      PRT;  2347 AA.
AC   Q8INH9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG7518-PB.
GN   ORFNames=CG7518;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003698; AAN14338.1; -.
DR   IntAct; Q8INH9; -.
DR   FlyBase; FBgn0038108; CG7518.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   PROSITE; PS00037; MYB_1; UNKNOWN_1.
SQ   SEQUENCE   2347 AA;  257013 MW;  23BF5FC5FFCAEA64 CRC64;

  Query Match             64.8%;  Score 46;  DB 2;  Length 2347;
  Best Local Similarity   73.3%;  Pred. No. 1.8e+02;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              :||| || :||||||
Db       1363 KAKKKEAKRAAAAAA 1377


RESULT 4
Q9VG05
ID   Q9VG05      PRELIMINARY;      PRT;  2451 AA.
AC   Q9VG05;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG7518-PA.
GN   ORFNames=CG7518;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
```

```
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003698; AAF54888.2; -.
DR   FlyBase; FBgn0038108; CG7518.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   PROSITE; PS00037; MYB_1; UNKNOWN_1.
SQ   SEQUENCE   2451 AA;  266959 MW;  088A2293F27481E2 CRC64;

  Query Match             64.8%;  Score 46;  DB 2;  Length 2451;
  Best Local Similarity   73.3%;  Pred. No. 1.9e+02;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              :||| || :||||||
Db       1363 KAKKKEAKRAAAAAA 1377


RESULT 5
Q6M9S8
ID   Q6M9S8      PRELIMINARY;      PRT;   847 AA.
AC   Q6M9S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=pc1947;
OS   Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC   Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX   NCBI_TaxID=264201;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA   Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA   Rattei T., Mewes H.-W., Wagner M.;
RT   "Genome sequence of an amoeba symbiont and its use for reconstructing
RT   the evolutionary history of chlamydiae.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX908798; CAF24671.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   847 AA;  97399 MW;  75C178870938FF21 CRC64;

  Query Match             63.4%;  Score 45;  DB 2;  Length 847;
  Best Local Similarity   80.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKA 10
              |||:|||||:
Db        723 EAKRYEAYKS 732


RESULT 6
Q6MBH0
ID   Q6MBH0      PRELIMINARY;      PRT;   867 AA.
AC   Q6MBH0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=pc1355;
OS   Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC   Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX   NCBI_TaxID=264201;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA   Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA   Rattei T., Mewes H.-W., Wagner M.;
RT   "Genome sequence of an amoeba symbiont and its use for reconstructing
```

```
RT   the evolutionary history of chlamydiae.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX908798; CAF24079.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   867 AA;  99667 MW;  84B67A53CD342E32 CRC64;

  Query Match            63.4%;  Score 45;  DB 2;  Length 867;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKA 10
              |||:|||||:
Db        739 EAKRYEAYKS 748


RESULT 7
Q8W0D1
ID   Q8W0D1      PRELIMINARY;      PRT;   380 AA.
AC   Q8W0D1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative nuclear RNA binding protein A.
GN   Name=P0690B02.20;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=12447438; DOI=10.1038/nature01184;
RA   Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA   Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA   Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA   Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA   Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA   Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA   Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA   Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA   Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA   Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA   Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA   Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA   Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA   Yano M., Jiang J., Gojobori T.;
RT   "The genome sequence and structure of rice chromosome 1.";
RL   Nature 420:312-316(2002).
DR   EMBL; AP003292; BAB84432.1; -.
DR   Gramene; Q8W0D1; -.
DR   Pfam; PF04774; HABP4_PAI-RBP1; 1.
SQ   SEQUENCE   380 AA;  40426 MW;  2B7C9916D9162194 CRC64;

  Query Match            62.0%;  Score 44;  DB 2;  Length 380;
  Best Local Similarity   78.6%;  Pred. No. 72;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              |:| || |||||||
Db         29 AQKAEAKKAAAAAA 42


RESULT 8
Q6I5H3
ID   Q6I5H3      PRELIMINARY;      PRT;   390 AA.
AC   Q6I5H3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein OSJNBa0053E05.13.
GN   Name=OSJNBa0053E05.13;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA   Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA   Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA   Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA   Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA   Wu H.-P., Shaw J.-F.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC121365; AAT47083.1; -.
DR   InterPro; IPR006861; HABP4_PAI-RBP1.
DR   Pfam; PF04774; HABP4_PAI-RBP1; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   390 AA;  41958 MW;  445445FF0E18B299 CRC64;

  Query Match            62.0%;  Score 44;  DB 2;  Length 390;
  Best Local Similarity   78.6%;  Pred. No. 73;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
              |:| || |||||||
Db         29 AQKAEAKKAAAAAA 42


RESULT 9
Q7S637
ID   Q7S637      PRELIMINARY;      PRT;   853 AA.
AC   Q7S637;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein B15B10.130.
GN   Name=NCU04772.1; Synonyms=B15B10.130;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   German Neurospora genome project;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000331; EAA30985.1; -.
DR   EMBL; BX897677; CAE85580.1; -.
```

```
KW   Hypothetical protein.
SQ   SEQUENCE   853 AA;  94019 MW;  505BF08C7CB6827D CRC64;

  Query Match             62.0%;  Score 44;  DB 2;  Length 853;
  Best Local Similarity   73.3%;  Pred. No. 1.5e+02;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EAKKYEAYKAAAAAA 15
              ||:| || | |||||
Db        671 EAEKEEAEKKAAAAA 685


RESULT 10
HXD8_CHICK
ID   HXD8_CHICK     STANDARD;      PRT;   188 AA.
AC   P23459;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Homeobox protein Hox-D8 (Chox-M).
GN   Name=HOXD8; Synonyms=CHOX-M;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91238215; PubMed=1674560;
RA   Crompton M.R., McGregor A.D., Goodwin G.H.;
RT   "cDNA cloning of a homeobox-containing gene expressed in avian
RT   myeloblastic virus-transformed chicken monoblastic leukaemia cells.";
RL   Leukemia 5:357-360(1991).
CC   -!- FUNCTION: Sequence-specific transcription factor which is part of
CC       a developmental regulatory system that provides cells with
CC       specific positional identities on the anterior-posterior axis.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the Antp homeobox family.
CC   -!- SIMILARITY: Contains 1 homeobox domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X57158; CAA40445.1; -.
DR   PIR; I50145; I50145.
DR   HSSP; P02833; 9ANT.
DR   TRANSFAC; T01754; -.
DR   InterPro; IPR001827; Antennapedia.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   InterPro; IPR000047; HTH_lambrepressr.
DR   Pfam; PF00046; Homeobox; 1.
DR   PRINTS; PR00025; ANTENNAPEDIA.
DR   PRINTS; PR00024; HOMEOBOX.
DR   PRINTS; PR00031; HTHREPRESSR.
DR   ProDom; PD000010; Homeobox; 1.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00032; ANTENNAPEDIA; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW   Transcription regulation.
FT   DOMAIN       15     25       Poly-Ala.
FT   SITE         83     88       Antp-type hexapeptide.
FT   DNA_BIND     95    154       Homeobox.
SQ   SEQUENCE   188 AA;  21729 MW;  D4560E8807FE29FE CRC64;

  Query Match             59.2%;  Score 42;  DB 1;  Length 188;
  Best Local Similarity   81.8%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 YEAYKAAAAAA 15
              | ||||||||
Db         10 YSKYKAAAAAA 20


RESULT 11
Q8S703
ID   Q8S703      PRELIMINARY;      PRT;   235 AA.
AC   Q8S703;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative glutathione S-transferase.
GN   Name=OSJNBa0034L04.24; ORFNames=OSJNBb0038A07.37;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22195796; PubMed=12207219; DOI=10.1007/s00438-002-0706-1;
RA   Yuan Q., Hill J., Hsiao J., Moffat K., Ouyang S., Cheng Z., Jiang J.,
RA   Buell C.R.;
RT   "Genome sequencing of a 239-kb region of rice chromosome 10L reveals a
RT   high frequency of gene duplication and a large chloroplast DNA
RT   insertion.";
RL   Mol. Genet. Genomics 267:713-720(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Buell R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA   Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA   Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA   Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA   Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   The Rice Chromosome 10 Sequencing Consortium;
RT   "In-depth view of structure, activity, and evolution of rice
RT   chromosome 10.";
RL   Science 300:1566-1569(2003).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the GST superfamily.
DR   EMBL; AC091680; AAM12328.1; -.
DR   EMBL; AC113948; AAM94508.1; -.
DR   EMBL; AE017114; AAP54743.1; -.
DR   HSSP; O04941; 1GWC.
DR   Gramene; Q8S703; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR004046; GST_Cterm.
DR   InterPro; IPR010987; GST_C_like.
DR   InterPro; IPR004045; GST_Nterm.
DR   Pfam; PF00043; GST_C; 1.
DR   Pfam; PF02798; GST_N; 1.
KW   Transferase.
SQ   SEQUENCE   235 AA;  25461 MW;  6FB0C8F156C8B45B CRC64;

  Query Match             59.2%;  Score 42;  DB 2;  Length 235;
  Best Local Similarity   71.4%;  Pred. No. 97;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AKKYEAYKAAAAAA 15
```

```
                ||| :| :||||||
Db        220 AKKRQAERAAAAAA 233


RESULT 12
HXD8_MOUSE
ID   HXD8_MOUSE     STANDARD;      PRT;   289 AA.
AC   P23463;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).
GN   Name=Hoxd8; Synonyms=Hox-4.3, Hoxd-8;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91209232; PubMed=1982431;
RA   Izpisua-Belmonte J.-C., Dolle P., Renucci A., Zappavigna V.,
RA   Falkenstein H., Duboule D.;
RT   "Primary structure and embryonic expression pattern of the mouse Hox-
RT   4.3 homeobox gene.";
RL   Development 110:733-745(1990).
RN   [2]
RP   SEQUENCE OF 191-289 FROM N.A.
RX   MEDLINE=91274361; PubMed=1675873; DOI=10.1016/0167-4781(91)90020-M;
RA   Sadoul R., Featherstone M.;
RT   "Sequence analysis of the homeobox-containing exon of the murine Hox-
RT   4.3 homeogene.";
RL   Biochim. Biophys. Acta 1089:259-261(1991).
RN   [3]
RP   SEQUENCE OF 195-254 FROM N.A.
RX   MEDLINE=92073356; PubMed=1683707;
RA   Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA   Copeland N.G., Potter S.S.;
RT   "Identification of 10 murine homeobox genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
RN   [4]
RP   SEQUENCE OF 192-260 FROM N.A.
RX   MEDLINE=92212934; PubMed=1348361;
RA   Nazarali A., Kim Y., Nirenberg M.;
RT   "Hox-1.11 and Hox-4.9 homeobox genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887(1992).
CC   -!- FUNCTION: Sequence-specific transcription factor which is part of
CC       a developmental regulatory system that provides cells with
CC       specific positional identities on the anterior-posterior axis.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the Antp homeobox family.
CC   -!- SIMILARITY: Contains 1 homeobox domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56561; CAA39911.1; -.
DR   EMBL; M87803; AAA37852.1; -.
DR   PIR; A43562; A43562.
DR   PIR; S16177; A41605.
DR   HSSP; P02833; 9ANT.
DR   TRANSFAC; T01426; -.
DR   MGD; MGI:96209; Hoxd8.
DR   InterPro; IPR001827; Antennapedia.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   Pfam; PF00046; Homeobox; 1.
DR   PRINTS; PR00025; ANTENNAPEDIA.
DR   PRINTS; PR00024; HOMEOBOX.
DR   ProDom; PD000010; Homeobox; 1.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00032; ANTENNAPEDIA; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW   Transcription regulation.
FT   DOMAIN       15     28       Poly-Ala.
FT   DOMAIN       62     89       Gly/Pro-rich.
FT   DOMAIN      108    117       Poly-Pro.
FT   SITE        183    188       Antp-type hexapeptide.
FT   DNA_BIND    195    254       Homeobox.
FT   CONFLICT    207    208       TL -> RV (in Ref. 1).
FT   CONFLICT    231    231       T -> S (in Ref. 1).
FT   CONFLICT    265    266       EA -> DG (in Ref. 1).
FT   CONFLICT    275    275       A -> V (in Ref. 2).
SQ   SEQUENCE   289 AA;  31410 MW;  5783099FB9B2BDFE CRC64;

  Query Match             59.2%;  Score 42;  DB 1;  Length 289;
  Best Local Similarity   81.8%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 YEAYKAAAAAA 15
              |  ||||||||
Db         10 YSKYKAAAAAA 20


RESULT 13
Q8IXZ1
ID   Q8IXZ1      PRELIMINARY;      PRT;   289 AA.
AC   Q8IXZ1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Homeo box D8.
GN   Name=HOXD8;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR   EMBL; BC038709; AAH38709.1; -.
DR   HSSP; P02833; 9ANT.
DR   GO; GO:0005634; C:nucleus; IEA.
```

```
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001827; Antennapedia.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   Pfam; PF00046; Homeobox; 1.
DR   PRINTS; PR00025; ANTENNAPEDIA.
DR   PRINTS; PR00024; HOMEOBOX.
DR   ProDom; PD000010; Homeobox; 1.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   DNA-binding; Homeobox; Nuclear protein.
SQ   SEQUENCE   289 AA;  31839 MW;  4C2621085174B447 CRC64;

  Query Match             59.2%;  Score 42;  DB 2;  Length 289;
  Best Local Similarity   81.8%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 YEAYKAAAAAA 15
              |  ||||||||
Db         10 YSKYKAAAAAA 20


RESULT 14
HXD8_HUMAN
ID   HXD8_HUMAN      STANDARD;      PRT;   290 AA.
AC   P13378;
DT   01-JAN-1990 (Rel. 13, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4).
GN   Name=HOXD8; Synonyms=HOX4E;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Birren B., Linton L., Nusbaum C., Lander E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;
RT   "A complete mutation analysis panel of human HOX genes.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 193-287 FROM N.A.
RX   MEDLINE=89306602; PubMed=2568311;
RA   Oliver G., Sidell N., Fiske N., Heinzmann C., Mohandas T.,
RA   Sparkes R.S., de Robertis E.M.;
RT   "Complementary homeo protein gradients in developing limb buds.";
RL   Genes Dev. 3:641-650(1989).
CC   -!- FUNCTION: Sequence-specific transcription factor which is part of
CC       a developmental regulatory system that provides cells with
CC       specific positional identities on the anterior-posterior axis.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the Antp homeobox family.
CC   -!- SIMILARITY: Contains 1 homeobox domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC009336; -; NOT_ANNOTATED_CDS.
DR   EMBL; AY014304; AAG42152.1; -.
DR   EMBL; AY014303; AAG42152.1; JOINED.
DR   EMBL; X15507; CAA33529.1; -.
DR   PIR; B32830; B32830.
DR   HSSP; P02833; 9ANT.
DR   TRANSFAC; T03332; -.
DR   Genew; HGNC:5139; HOXD8.
DR   MIM; 142985; -.
DR   GO; GO:0005634; C:nucleus; NAS.
DR   GO; GO:0003700; F:transcription factor activity; NAS.
DR   GO; GO:0008595; P:determination of anterior/posterior axis, e. . .; NAS.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR   InterPro; IPR001827; Antennapedia.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR009057; Homeodomain_like.
DR   Pfam; PF00046; Homeobox; 1.
DR   PRINTS; PR00025; ANTENNAPEDIA.
DR   PRINTS; PR00024; HOMEOBOX.
DR   ProDom; PD000010; Homeobox; 1.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00032; ANTENNAPEDIA; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW   Transcription regulation.
FT   DOMAIN       15     23       Poly-Ala.
FT   DOMAIN       45     50       Poly-Ala.
FT   DOMAIN      109    123       Poly-Pro.
FT   DNA_BIND    197    256       Homeobox.
FT   CONFLICT    287    287       G -> A (in Ref. 3).
SQ   SEQUENCE   290 AA;  31910 MW;  75FF95A73E2AA85F CRC64;

  Query Match             59.2%;  Score 42;  DB 1;  Length 290;
  Best Local Similarity   81.8%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 YEAYKAAAAAA 15
              |  ||||||||
Db         10 YSKYKAAAAAA 20


RESULT 15
Q6AY89
ID   Q6AY89      PRELIMINARY;      PRT;   364 AA.
AC   Q6AY89;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC079147; AAH79147.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003697; F:single-stranded DNA binding; IEA.
DR GO; GO:0030528; F:transcription regulator activity; IEA.
DR InterPro; IPR006594; LisH.
DR InterPro; IPR007591; SSDP.
DR InterPro; IPR008116; SSDP_DNA_bind.
DR Pfam; PF04503; SSDP; 1.
DR PRINTS; PR01743; SSDNABINDING.
DR SMART; SM00667; LisH; 1.
DR PROSITE; PS50896; LISH; 1.
KW Hypothetical protein.
SQ SEQUENCE 364 AA; 37518 MW; A31EEB7AC4F58A78 CRC64;

Query Match 59.2%; Score 42; DB 2; Length 364;
Best Local Similarity 64.3%; Pred. No. 1.4e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 EAKKYEAYKAAAAA 14
              ||| :: | |||||
Db         85 EAKVFQDYSAAAAA 98
```

Search completed: April 4, 2005, 17:31:07
Job time : 114.094 secs

OM protein - protein search, using sw model

Run on: April 4, 2005, 16:53:02 ; Search time 132.812 Seconds
(without alignments)
49.505 Million cell updates/sec

Title: US-10-056-583A-96
Perfect score: 83
Sequence: 1 APEKAKFEAFKAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	17	5	ABP52302	Abp52302 HLA-DR2 m
2	80	96.4	17	5	ABP52303	Abp52303 HLA-DR2 m
3	69	83.1	17	5	ABP52294	Abp52294 HLA-DR2 m
4	69	83.1	19	5	ABP52295	Abp52295 HLA-DR2 m
5	64	77.1	15	5	ABP52301	Abp52301 HLA-DR2 m
6	64	77.1	15	5	ABP52297	Abp52297 HLA-DR2 m
7	61	73.5	15	5	ABP52291	Abp52291 HLA-DR2 m
8	58	69.9	15	5	ABP52271	Abp52271 HLA-DR2 m
9	58	69.9	15	5	ABP52298	Abp52298 HLA-DR2 m
10	58	69.9	15	5	ABP52300	Abp52300 HLA-DR2 m
11	58	69.9	15	5	ABP52304	Abp52304 HLA-DR2 m
12	58	69.9	17	5	ABP52296	Abp52296 HLA-DR2 m
13	57	68.7	15	5	ABP52299	Abp52299 HLA-DR2 m
14	55	66.3	15	5	ABP52290	Abp52290 HLA-DR2 m
15	55	66.3	15	5	ABP52292	Abp52292 HLA-DR2 m
16	52	62.7	15	5	ABP52270	Abp52270 HLA-DR2 m
17	51	61.4	15	5	ABP52305	Abp52305 HLA-DR2 m
18	50	60.2	572	4	ABB59072	Abb59072 Drosophil
19	48	57.8	15	5	ABP52263	Abp52263 HLA-DR2 m
20	47	56.6	15	5	ABP52272	Abp52272 HLA-DR2 m
21	46	55.4	15	5	ABP52259	Abp52259 HLA-DR2 m
22	46	55.4	15	5	ABP52257	Abp52257 HLA-DR2 m
23	46	55.4	203	8	ADS30243	Ads30243 Bacterial
24	46	55.4	465	6	ABU38244	Abu38244 Protein e
25	46	55.4	469	7	ABO79123	Abo79123 Pseudomon
26	45	54.2	15	5	ABP52289	Abp52289 HLA-DR2 m
27	44	53.0	21	2	AAW19062	Aaw19062 Trypanoso
28	44	53.0	21	2	AAW19087	Aaw19087 Trypanoso
29	44	53.0	21	2	AAY32839	Aay32839 TcE repea
30	44	53.0	21	2	AAY23311	Aay23311 Epitope o
31	44	53.0	21	2	AAY23313	Aay23313 Repeat se
32	44	53.0	21	3	AAB26466	Aab26466 T.cruzi T
33	44	53.0	21	3	AAB26468	Aab26468 T.cruzi s
34	44	53.0	145	3	AAB32749	Aab32749 Eucalyptu
35	44	53.0	262	2	AAW06913	Aaw06913 T. cruzi
36	44	53.0	262	2	AAY32848	Aay32848 TcE prote
37	44	53.0	263	2	AAY23306	Aay23306 TcE antig
38	43	51.8	15	5	ABP52253	Abp52253 HLA-DR2 m
39	43	51.8	15	5	ABP52251	Abp52251 HLA-DR2 m
40	43	51.8	15	5	ABP52239	Abp52239 HLA-DR2 m
41	43	51.8	351	6	ABU35314	Abu35314 Protein e
42	43	51.8	397	6	ABO00558	Abo00558 Novel hum
43	43	51.8	1512	7	ADE47702	Ade47702 Human NOV
44	43	51.8	1512	8	ADJ78972	Adj78972 Human NOV
45	42	50.6	15	5	ABP52261	Abp52261 HLA-DR2 m

ALIGNMENTS

RESULT 1
ABP52302
ID ABP52302 standard; peptide; 17 AA.
XX
AC ABP52302;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APEKAKFEAFKAAAAPA 17
||||||||||||||||
Db 1 APEKAKFEAFKAAAAPA 17

RESULT 2
ABP52303
ID ABP52303 standard; peptide; 17 AA.
XX
AC ABP52303;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 96.4%; Score 80; DB 5; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APEKAKFEAFKAAAAPA 17
||||||||:|||||||
Db 1 APEKAKFEAYKAAAAPA 17

RESULT 3
ABP52294
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 83.1%; Score 69; DB 5; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00023;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APEKAKFEAFKAAAAPA 17

```
                  ||||||:||:||||| |
Db          1 APEKAKYEAYKAAAAAA 17


RESULT 4
ABP52295
ID   ABP52295 standard; peptide; 19 AA.
XX
AC   ABP52295;
XX
DT   16-OCT-2002  (first entry)
XX
DE   HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
KW   Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW   HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW   immune response; antiinflammatory; neuroprotective; proliferation;
KW   MHC class II protein inhibitor; demyelinating disease; inhibition;
KW   post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW   anti-tumour necrosis factor agent.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200259143-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-US002071.
XX
PR   24-JAN-2001; 2001US-0263569P.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Strominger JL,  Fridkis-Hareli M;
XX
DR   WPI; 2002-608439/65.
XX
PT   New compositions comprising synthetic peptides in complex with a major
PT   histocompatibility complex class II HLADR2 protein, useful for treating a
PT   demyelinating disease, e.g. multiple sclerosis, or post-viral
PT   encephalomyelitis.
XX
PS   Claim 28; Page 39; 54pp; English.
XX
CC   The present invention describes compositions (I) comprising a peptide
CC   with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC   residues. The complex of the peptide with a major histocompatibility
CC   complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC   immune response. (I) has antiinflammatory and neuroprotective activities,
CC   and can be used as a MHC class II protein inhibitor. The compositions
CC   comprising the peptides are useful for treating demyelinating diseases
CC   such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC   demyelinating condition, and a side effect of administering an anti-
CC   tumour necrosis factor agents. The peptide further inhibits proliferation
CC   of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC   ABP52305 represent peptides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 19 AA;

  Query Match             83.1%;  Score 69;  DB 5;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 0.00026;
  Matches   14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
                ||||||:||:||||| |
Db          1 APEKAKYEAYKAAAAAA 17


RESULT 5
ABP52301
ID   ABP52301 standard; peptide; 15 AA.
XX
AC   ABP52301;
XX
DT   16-OCT-2002  (first entry)
XX
DE   HLA-DR2 molecule binding peptide SEQ ID NO:95.
XX
KW   Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW   HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW   immune response; antiinflammatory; neuroprotective; proliferation;
KW   MHC class II protein inhibitor; demyelinating disease; inhibition;
KW   post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW   anti-tumour necrosis factor agent.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200259143-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-US002071.
XX
PR   24-JAN-2001; 2001US-0263569P.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Strominger JL,  Fridkis-Hareli M;
XX
DR   WPI; 2002-608439/65.
XX
PT   New compositions comprising synthetic peptides in complex with a major
PT   histocompatibility complex class II HLADR2 protein, useful for treating a
PT   demyelinating disease, e.g. multiple sclerosis, or post-viral
PT   encephalomyelitis.
XX
PS   Claim 28; Page 39; 54pp; English.
XX
CC   The present invention describes compositions (I) comprising a peptide
CC   with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC   residues. The complex of the peptide with a major histocompatibility
CC   complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC   immune response. (I) has antiinflammatory and neuroprotective activities,
CC   and can be used as a MHC class II protein inhibitor. The compositions
CC   comprising the peptides are useful for treating demyelinating diseases
CC   such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC   demyelinating condition, and a side effect of administering an anti-
CC   tumour necrosis factor agents. The peptide further inhibits proliferation
CC   of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC   ABP52305 represent peptides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 15 AA;

  Query Match             77.1%;  Score 64;  DB 5;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 0.0013;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
                ||||||||||||| |
Db          1 EKAKFEAFKAAAAAA 15


RESULT 6
ABP52297
ID   ABP52297 standard; peptide; 15 AA.
XX
AC   ABP52297;
XX
DT   16-OCT-2002  (first entry)
XX
DE   HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
```

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 77.1%; Score 64; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0013;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
|| ||||:|||||||
Db 1 EKPKFEAYKAAAAPA 15

RESULT 7
ABP52291
ID ABP52291 standard; peptide; 15 AA.
XX
AC ABP52291;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:85.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 73.5%; Score 61; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
|| |:||:|||||||
Db 1 EKPKYEAYKAAAAPA 15

RESULT 8
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX

PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 69.9%; Score 58; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.013;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
||||:||:||||| |
Db 1 EKAKYEAYKAAAAAA 15

RESULT 9
ABP52298
ID ABP52298 standard; peptide; 15 AA.
XX
AC ABP52298;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 69.9%; Score 58; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.013;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
||||:||:||||| |
Db 1 EKAKYEAYKAAAAAA 15

RESULT 10
ABP52300
ID ABP52300 standard; peptide; 15 AA.
XX
AC ABP52300;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:94.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 69.9%; Score 58; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.013;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
|| | ||||||||||
Db 1 EKPKEEAFKAAAAPA 15

RESULT 11
ABP52304
ID ABP52304 standard; peptide; 15 AA.
XX
AC ABP52304;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:98.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 69.9%; Score 58; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
| ||||:|||||||
Db 1 EAPKFEAYKAAAAPA 15

RESULT 12
ABP52296
ID ABP52296 standard; peptide; 17 AA.
XX
AC ABP52296;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

```
CC   ABP52305 represent peptides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 AA;

  Query Match             69.9%;  Score 58;  DB 5;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 0.015;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              ||||:||:||||| |
Db          1 EKAKYEAYKAAAAAA 15


RESULT 13
ABP52299
ID   ABP52299 standard; peptide; 15 AA.
XX
AC   ABP52299;
XX
DT   16-OCT-2002  (first entry)
XX
DE   HLA-DR2 molecule binding peptide SEQ ID NO:93.
XX
KW   Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW   HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW   immune response; antiinflammatory; neuroprotective; proliferation;
KW   MHC class II protein inhibitor; demyelinating disease; inhibition;
KW   post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW   anti-tumour necrosis factor agent.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200259143-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-US002071.
XX
PR   24-JAN-2001; 2001US-0263569P.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Strominger JL,  Fridkis-Hareli M;
XX
DR   WPI; 2002-608439/65.
XX
PT   New compositions comprising synthetic peptides in complex with a major
PT   histocompatibility complex class II HLADR2 protein, useful for treating a
PT   demyelinating disease, e.g. multiple sclerosis, or post-viral
PT   encephalomyelitis.
XX
PS   Claim 28; Page 39; 54pp; English.
XX
CC   The present invention describes compositions (I) comprising a peptide
CC   with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC   residues. The complex of the peptide with a major histocompatibility
CC   complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC   immune response. (I) has antiinflammatory and neuroprotective activities,
CC   and can be used as a MHC class II protein inhibitor. The compositions
CC   comprising the peptides are useful for treating demyelinating diseases
CC   such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC   demyelinating condition, and a side effect of administering an anti-
CC   tumour necrosis factor agents. The peptide further inhibits proliferation
CC   of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC   ABP52305 represent peptides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 15 AA;

  Query Match             68.7%;  Score 57;  DB 5;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 0.019;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              || | ||:|||||||
Db          1 EKPKVEAYKAAAAPA 15


RESULT 14
ABP52290
ID   ABP52290 standard; peptide; 15 AA.
XX
AC   ABP52290;
XX
DT   16-OCT-2002  (first entry)
XX
DE   HLA-DR2 molecule binding peptide SEQ ID NO:84.
XX
KW   Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW   HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW   immune response; antiinflammatory; neuroprotective; proliferation;
KW   MHC class II protein inhibitor; demyelinating disease; inhibition;
KW   post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW   anti-tumour necrosis factor agent.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200259143-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-US002071.
XX
PR   24-JAN-2001; 2001US-0263569P.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Strominger JL,  Fridkis-Hareli M;
XX
DR   WPI; 2002-608439/65.
XX
PT   New compositions comprising synthetic peptides in complex with a major
PT   histocompatibility complex class II HLADR2 protein, useful for treating a
PT   demyelinating disease, e.g. multiple sclerosis, or post-viral
PT   encephalomyelitis.
XX
PS   Claim 28; Page 39; 54pp; English.
XX
CC   The present invention describes compositions (I) comprising a peptide
CC   with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC   residues. The complex of the peptide with a major histocompatibility
CC   complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC   immune response. (I) has antiinflammatory and neuroprotective activities,
CC   and can be used as a MHC class II protein inhibitor. The compositions
CC   comprising the peptides are useful for treating demyelinating diseases
CC   such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC   demyelinating condition, and a side effect of administering an anti-
CC   tumour necrosis factor agents. The peptide further inhibits proliferation
CC   of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC   ABP52305 represent peptides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 15 AA;

  Query Match             66.3%;  Score 55;  DB 5;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 0.04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              |  |:||:|||||||
Db          1 EAPKYEAYKAAAAPA 15
```

RESULT 15
ABP52292
ID ABP52292 standard; peptide; 15 AA.
XX
AC ABP52292;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLADR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 66.3%; Score 55; DB 5; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 EKAKFEAFKAAAAPA 17
              |  |:||:|||||||
Db          1 EAPKYEAYKAAAAPA 15
```

Search completed: April 4, 2005, 17:26:04
Job time : 133.812 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:27:14 ; Search time 31.3438 Seconds
(without alignments)
40.488 Million cell updates/sec

Title: US-10-056-583A-96
Perfect score: 83
Sequence: 1 APEKAKFEAFKAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	55.4	212	4	US-09-902-540-16451	Sequence 16451, A
2	46	55.4	469	4	US-09-252-991A-27869	Sequence 27869, A
3	44	53.0	21	2	US-08-557-309B-58	Sequence 58, Appl
4	44	53.0	21	2	US-08-929-414-11	Sequence 11, Appl
5	44	53.0	21	3	US-08-834-306-56	Sequence 56, Appl
6	44	53.0	21	3	US-08-834-306-58	Sequence 58, Appl
7	44	53.0	21	3	US-08-993-674A-56	Sequence 56, Appl
8	44	53.0	21	3	US-08-993-674A-58	Sequence 58, Appl
9	44	53.0	21	4	US-09-256-976-56	Sequence 56, Appl
10	44	53.0	21	4	US-09-256-976-58	Sequence 58, Appl
11	44	53.0	145	4	US-09-640-211A-798	Sequence 798, App
12	44	53.0	262	1	US-08-403-379A-1	Sequence 1, Appli
13	44	53.0	262	2	US-08-929-414-1	Sequence 1, Appli
14	44	53.0	263	2	US-08-557-309B-51	Sequence 51, Appl
15	44	53.0	263	3	US-08-834-306-51	Sequence 51, Appl
16	44	53.0	263	3	US-08-993-674A-51	Sequence 51, Appl
17	44	53.0	263	4	US-09-256-976-51	Sequence 51, Appl
18	42	50.6	162	4	US-09-732-210-1445	Sequence 1445, Ap
19	42	50.6	324	4	US-09-248-796A-17156	Sequence 17156, A
20	41	49.4	21	2	US-08-557-309B-61	Sequence 61, Appl
21	41	49.4	21	2	US-08-929-414-13	Sequence 13, Appl
22	41	49.4	21	3	US-08-834-306-60	Sequence 60, Appl
23	41	49.4	21	3	US-08-993-674A-60	Sequence 60, Appl
24	41	49.4	21	4	US-09-256-976-60	Sequence 60, Appl
25	41	49.4	642	4	US-09-489-039A-12434	Sequence 12434, A
26	40	48.2	21	1	US-08-403-379A-3	Sequence 3, Appli
27	40	48.2	21	2	US-08-557-309B-52	Sequence 52, Appl
28	40	48.2	21	2	US-08-557-309B-57	Sequence 57, Appl
29	40	48.2	21	2	US-08-557-309B-60	Sequence 60, Appl
30	40	48.2	21	2	US-08-929-414-3	Sequence 3, Appli
31	40	48.2	21	2	US-08-929-414-10	Sequence 10, Appl
32	40	48.2	21	2	US-08-929-414-12	Sequence 12, Appl
33	40	48.2	21	3	US-08-834-306-55	Sequence 55, Appl
34	40	48.2	21	3	US-08-834-306-59	Sequence 59, Appl
35	40	48.2	21	3	US-08-993-674A-55	Sequence 55, Appl
36	40	48.2	21	3	US-08-993-674A-59	Sequence 59, Appl
37	40	48.2	21	3	US-09-248-588-46	Sequence 46, Appl
38	40	48.2	21	4	US-09-256-976-55	Sequence 55, Appl
39	40	48.2	21	4	US-09-256-976-59	Sequence 59, Appl
40	40	48.2	85	4	US-09-256-976-82	Sequence 82, Appl
41	40	48.2	94	4	US-09-256-976-95	Sequence 95, Appl
42	40	48.2	214	4	US-09-252-991A-31304	Sequence 31304, A
43	40	48.2	219	2	US-08-557-309B-54	Sequence 54, Appl
44	40	48.2	419	4	US-09-489-039A-13260	Sequence 13260, A
45	40	48.2	442	3	US-08-834-306-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-902-540-16451
; Sequence 16451, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16451
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16451

Query Match 55.4%; Score 46; DB 4; Length 212;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 PEKAKFEAFKAAAAP 16
              |::| |:|  |||||
Db        134 PDQAPFDAILAAAAP 148
```

RESULT 2
US-09-252-991A-27869
; Sequence 27869, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27869
; LENGTH: 469
; TYPE: PRT

```
;  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27869

  Query Match             55.4%;  Score 46;  DB 4;  Length 469;
  Best Local Similarity   62.5%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAPA 17
              |    || ||||| ||
Db        176 PNALAFERFKAAAYPA 191


RESULT 3
US-08-557-309B-58
; Sequence 58, Application US/08557309B
; Patent No. 5916572
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Houghton, Raymond L.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND   PREVENTION OF T
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,309B
;      FILING DATE:  14-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.422
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-557-309B-58

  Query Match             53.0%;  Score 44;  DB 2;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 4
US-08-929-414-11
; Sequence 11, Application US/08929414
; Patent No. 5942403
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Haughton, Raymond
;    APPLICANT:  Skeiky, Yasir A.W.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION
;    TITLE OF INVENTION:  OF T. CRUZI INFECTION
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/929,414
;      FILING DATE:  15-SEP-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.406C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-929-414-11

  Query Match             53.0%;  Score 44;  DB 2;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 5
US-08-834-306-56
; Sequence 56, Application US/08834306
; Patent No. 6054135
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Houghton, Raymond L.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND   PREVENTION OF T
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,306
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.422C1
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-834-306-56

  Query Match             53.0%;  Score 44;  DB 3;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 6
US-08-834-306-58
; Sequence 58, Application US/08834306
; Patent No. 6054135
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Houghton, Raymond L.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND   PREVENTION OF T
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,306
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.422C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-834-306-58

  Query Match             53.0%;  Score 44;  DB 3;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 7
US-08-993-674A-56
; Sequence 56, Application US/08993674A
; Patent No. 6228372
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Houghton, Raymond L.
;    APPLICANT:  Smith, John M.
;    APPLICANT:  McNeill, Patricia D.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND   PREVENTION OF T
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/993,674A
;      FILING DATE:  18-DEC-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.422C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-993-674A-56

  Query Match             53.0%;  Score 44;  DB 3;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 8
US-08-993-674A-58
; Sequence 58, Application US/08993674A
; Patent No. 6228372
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Houghton, Raymond L.
;    APPLICANT:  Smith, John M.
;    APPLICANT:  McNeill, Patricia D.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND   PREVENTION OF T
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/993,674A
;       FILING DATE:  18-DEC-1997
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maki, David J.
;       REGISTRATION NUMBER:  31,392
;       REFERENCE/DOCKET NUMBER:  210121.422C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
US-08-993-674A-58

  Query Match             53.0%;  Score 44;  DB 3;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 9
US-09-256-976-56
; Sequence 56, Application US/09256976
; Patent No. 6419933
; GENERAL INFORMATION:
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Skeiky, Yasir A.W.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT: Smith, John M.
;  APPLICANT: McNeill, Patricia D.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
;  TITLE OF INVENTION: OF T. CRUZI INFECTION
;  FILE REFERENCE: 210121.422C3
;  CURRENT APPLICATION NUMBER: US/09/256,976
;  CURRENT FILING DATE: 1999-02-24
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  TcE antigenic
;   OTHER INFORMATION: epitope
US-09-256-976-56

  Query Match             53.0%;  Score 44;  DB 4;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 10
US-09-256-976-58
; Sequence 58, Application US/09256976
; Patent No. 6419933
; GENERAL INFORMATION:
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Skeiky, Yasir A.W.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT: Smith, John M.
;  APPLICANT: McNeill, Patricia D.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
;  TITLE OF INVENTION: OF T. CRUZI INFECTION
;  FILE REFERENCE: 210121.422C3
;  CURRENT APPLICATION NUMBER: US/09/256,976
;  CURRENT FILING DATE: 1999-02-24
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  TcE
;   OTHER INFORMATION: antigenic epitope
US-09-256-976-58

  Query Match             53.0%;  Score 44;  DB 4;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 0.78;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          5 APAKAAAAPAKAAAAPA 21


RESULT 11
US-09-640-211A-798
; Sequence 798, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
;  APPLICANT: Wood, Marion
;  APPLICANT:  Shenk, Michael A.
;  APPLICANT:  McGrath, Annette
;  APPLICANT:  Glenn, Matthew
;  TITLE OF INVENTION: Compositions and Methods for the
;  TITLE OF INVENTION:  Modification of Gene Transcription
;  FILE REFERENCE: 11000.1021C1U
;  CURRENT APPLICATION NUMBER: US/09/640,211A
;  CURRENT FILING DATE:  2000-08-16
;  NUMBER OF SEQ ID NOS: 2368
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 798
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: Eucalyptus grandis
US-09-640-211A-798

  Query Match             53.0%;  Score 44;  DB 4;  Length 145;
  Best Local Similarity   64.7%;  Pred. No. 6.4;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              ||  | | |  ||||||
Db        113 APIPASFSAPSAAAAPA 129


RESULT 12
US-08-403-379A-1
; Sequence 1, Application US/08403379A
; Patent No. 5756662
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION
;    TITLE OF INVENTION:  OF T. CRUZI INFECTION
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
```

```
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,379A
;      FILING DATE:  14-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-403-379A-1

  Query Match             53.0%;  Score 44;  DB 1;  Length 262;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db        141 APAKAAAAPAKAAAAPA 157


RESULT 13
US-08-929-414-1
; Sequence 1, Application US/08929414
; Patent No. 5942403
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Haughton, Raymond
;    APPLICANT:  Skeiky, Yasir A.W.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION
;    TITLE OF INVENTION:  OF T. CRUZI INFECTION
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/929,414
;      FILING DATE:  15-SEP-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.406C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-929-414-1

  Query Match             53.0%;  Score 44;  DB 2;  Length 262;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db        141 APAKAAAAPAKAAAAPA 157


RESULT 14
US-08-557-309B-51
; Sequence 51, Application US/08557309B
; Patent No. 5916572
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Houghton, Raymond L.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND  PREVENTION OF T
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,309B
;      FILING DATE:  14-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.422
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-557-309B-51

  Query Match             53.0%;  Score 44;  DB 2;  Length 263;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db        142 APAKAAAAPAKAAAAPA 158


RESULT 15
US-08-834-306-51
; Sequence 51, Application US/08834306
; Patent No. 6054135
;  GENERAL INFORMATION:
;    APPLICANT:  Reed,Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Lodes, Michael J.
```

```
;    APPLICANT:  Houghton, Raymond L.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DETECTION AND   PREVENTION OF T
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,306
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.422C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-834-306-51

  Query Match             53.0%;  Score 44;  DB 3;  Length 263;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db        142 APAKAAAAPAKAAAAPA 158


Search completed: April  4, 2005, 17:47:40
Job time : 32.3438 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:21:54 ; Search time 100.406 Seconds
(without alignments)
56.143 Million cell updates/sec

Title: US-10-056-583A-96
Perfect score: 83
Sequence: 1 APEKAKFEAFKAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	17	14	US-10-056-583-96	Sequence 96, Appl
2	80	96.4	17	14	US-10-056-583-97	Sequence 97, Appl
3	69	83.1	17	14	US-10-056-583-88	Sequence 88, Appl
4	69	83.1	19	14	US-10-056-583-89	Sequence 89, Appl
5	64	77.1	15	14	US-10-056-583-91	Sequence 91, Appl
6	64	77.1	15	14	US-10-056-583-95	Sequence 95, Appl
7	61	73.5	15	14	US-10-056-583-85	Sequence 85, Appl
8	58	69.9	15	14	US-10-056-583-65	Sequence 65, Appl
9	58	69.9	15	14	US-10-056-583-94	Sequence 94, Appl
10	58	69.9	15	14	US-10-056-583-98	Sequence 98, Appl
11	58	69.9	17	14	US-10-056-583-90	Sequence 90, Appl
12	57	68.7	15	14	US-10-056-583-93	Sequence 93, Appl
13	55	66.3	15	14	US-10-056-583-84	Sequence 84, Appl
14	55	66.3	15	14	US-10-056-583-86	Sequence 86, Appl
15	52	62.7	15	14	US-10-056-583-64	Sequence 64, Appl
16	52	62.7	15	14	US-10-056-583-92	Sequence 92, Appl
17	51	61.4	15	14	US-10-056-583-99	Sequence 99, Appl
18	48	57.8	15	14	US-10-056-583-57	Sequence 57, Appl
19	47	56.6	15	14	US-10-056-583-66	Sequence 66, Appl
20	46	55.4	15	14	US-10-056-583-51	Sequence 51, Appl
21	46	55.4	15	14	US-10-056-583-53	Sequence 53, Appl
22	46	55.4	203	15	US-10-369-493-19276	Sequence 19276, A
23	46	55.4	465	15	US-10-282-122A-66168	Sequence 66168, A
24	45	54.2	15	14	US-10-056-583-83	Sequence 83, Appl
25	44	53.0	113	15	US-10-425-114-70689	Sequence 70689, A
26	44	53.0	386	16	US-10-437-963-194029	Sequence 194029,
27	43	51.8	15	14	US-10-056-583-33	Sequence 33, Appl
28	43	51.8	15	14	US-10-056-583-45	Sequence 45, Appl
29	43	51.8	15	14	US-10-056-583-47	Sequence 47, Appl
30	43	51.8	121	16	US-10-767-701-49020	Sequence 49020, A
31	43	51.8	351	15	US-10-282-122A-63238	Sequence 63238, A
32	43	51.8	397	15	US-10-243-552-360	Sequence 360, App
33	43	51.8	1512	15	US-10-210-130-64	Sequence 64, Appl
34	42	50.6	15	14	US-10-056-583-38	Sequence 38, Appl
35	42	50.6	15	14	US-10-056-583-55	Sequence 55, Appl
36	42	50.6	15	14	US-10-056-583-56	Sequence 56, Appl
37	42	50.6	15	14	US-10-056-583-63	Sequence 63, Appl
38	42	50.6	162	15	US-10-282-122A-62570	Sequence 62570, A
39	42	50.6	162	15	US-10-282-122A-64801	Sequence 64801, A
40	42	50.6	180	15	US-10-424-599-266399	Sequence 266399,
41	42	50.6	421	15	US-10-282-122A-56483	Sequence 56483, A
42	42	50.6	570	15	US-10-094-749-3117	Sequence 3117, Ap
43	42	50.6	570	16	US-10-408-765A-2514	Sequence 2514, Ap
44	41.5	50.0	307	16	US-10-469-061A-45	Sequence 45, Appl
45	41.5	50.0	307	16	US-10-469-061A-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match 100.0%; Score 83; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APEKAKFEAFKAAAAPA 17
||||||||||||||||
Db 1 APEKAKFEAFKAAAAPA 17

RESULT 2
US-10-056-583-97

```
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

  Query Match             96.4%;  Score 80;  DB 14;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e-06;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              |||||||||:|||||||
Db          1 APEKAKFEAYKAAAAPA 17


RESULT 3
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

  Query Match             83.1%;  Score 69;  DB 14;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 0.00012;
  Matches   14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              ||||||:||:||||| |
Db          1 APEKAKYEAYKAAAAAA 17


RESULT 4
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89

  Query Match             83.1%;  Score 69;  DB 14;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 0.00014;
  Matches   14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              ||||||:||:||||| |
Db          1 APEKAKYEAYKAAAAAA 17


RESULT 5
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

  Query Match             77.1%;  Score 64;  DB 14;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 0.00071;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              || ||||:|||||||
Db          1 EKPKFEAYKAAAAPA 15


RESULT 6
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
```

```
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

  Query Match             77.1%;  Score 64;  DB 14;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 0.00071;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              |||||||||||||| |
Db          1 EKAKFEAFKAAAAAA 15


RESULT 7
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

  Query Match             73.5%;  Score 61;  DB 14;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 0.0022;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              || |:||:|||||||
Db          1 EKPKYEAYKAAAAPA 15


RESULT 8
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

  Query Match             69.9%;  Score 58;  DB 14;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 0.007;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              ||||:||:||||| |
Db          1 EKAKYEAYKAAAAAA 15


RESULT 9
US-10-056-583-94
; Sequence 94, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94

  Query Match             69.9%;  Score 58;  DB 14;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 0.007;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              || | ||||||||||
Db          1 EKPKEEAFKAAAAPA 15


RESULT 10
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98

Query Match 69.9%; Score 58; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
| |||:|||||||
Db 1 EAPKFEAYKAAAAPA 15

RESULT 11
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

Query Match 69.9%; Score 58; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0081;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
||||:||:||||| |
Db 1 EKAKYEAYKAAAAAA 15

RESULT 12
US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-93

Query Match 68.7%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.01;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
|| | ||:|||||||
Db 1 EKPKVEAYKAAAAPA 15

RESULT 13
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match 66.3%; Score 55; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.022;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
| |:||:|||||||
Db 1 EAPKYEAYKAAAAPA 15

RESULT 14
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match 66.3%; Score 55; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.022;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKFEAFKAAAAPA 17
| |:||:|||||||
Db 1 EAPKYEAYKAAAAPA 15

```
RESULT 15
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
;  APPLICANT: Presidents and Fellows of Harvard College
;  APPLICANT:  Strominger, Jack L.
;  APPLICANT:  Fridkis-Hareli, Masha
;  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 24655-017
;  CURRENT APPLICATION NUMBER: US/10/056,583
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: 60/263,569
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

  Query Match             62.7%;  Score 52;  DB 14;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 0.069;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 EKAKFEAFKAAAAPA 17
              | ||:||:||||| |
Db          1 EAAKYEAYKAAAAAA 15


Search completed: April  4, 2005, 17:34:53
Job time : 101.406 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:01:24 ; Search time 28.1562 Seconds
(without alignments)
58.093 Million cell updates/sec

Title: US-10-056-583A-96
Perfect score: 83
Sequence: 1 APEKAKFEAFKAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	57.8	389	2	G87332	hypothetical prote
2	46	55.4	465	2	D83598	probable zinc prot
3	45.5	54.8	189	2	S77930	exoskeletal protei
4	45.5	54.8	189	2	S77935	exoskeletal protei
5	45	54.2	179	2	F97683	50S ribosomal prot
6	45	54.2	179	2	AF2908	50S ribosomal prot
7	44	53.0	97	2	G60110	repetitive protein
8	44	53.0	408	2	AH3269	dihydrolipoamide S
9	43	51.8	128	2	T40464	probable RNA bindi
10	42	50.6	84	2	T23177	hypothetical prote
11	42	50.6	162	2	H70927	probable rpsP prot
12	42	50.6	421	2	JV0057	tolA protein - Esc
13	42	50.6	743	2	F71062	hypothetical prote
14	41	49.4	405	2	AH2752	dihydrolipoamide a
15	41	49.4	447	2	AB3359	dihydrolipoamide S
16	41	49.4	457	2	F97533	dihydrolipoamide a
17	41	49.4	565	2	C87278	hypothetical prote
18	41	49.4	629	2	AH0521	dihydrolipoamide a
19	41	49.4	828	2	F96535	hypothetical prote
20	40	48.2	73	2	S40015	phd protein - phag
21	40	48.2	136	2	AI0026	50S ribosomal prot
22	40	48.2	143	2	A87678	hypothetical prote
23	40	48.2	306	2	G96014	hypothetical prote
24	40	48.2	321	2	T07922	probable 1-aminocy
25	40	48.2	416	2	AB1609	branched-chain alp
26	40	48.2	507	1	NNBY1	anthranilate synth
27	40	48.2	704	2	B83914	beta-xylosidase (1
28	40	48.2	1020	1	QFHUH	neurofilament trip
29	40	48.2	1132	2	C75259	probable iron-sulf
30	39	47.0	106	2	A81203	conserved hypothet
31	39	47.0	117	2	C81779	hypothetical prote
32	39	47.0	129	1	TNLJG3	trans-activating t
33	39	47.0	136	1	R5EC16	ribosomal protein
34	39	47.0	136	2	AH1006	50S ribosomal chai
35	39	47.0	136	2	F85996	50S ribosomal subu
36	39	47.0	136	2	B91151	50S ribosomal subu
37	39	47.0	151	1	HSWT2A	histone H2A.2 - wh
38	39	47.0	184	2	D83234	hypothetical prote
39	39	47.0	196	2	E97352	transcription regu
40	39	47.0	198	2	AI2622	conserved hypothet
41	39	47.0	217	2	A97405	hypothetical prote
42	39	47.0	329	2	D96030	hypothetical prote
43	39	47.0	338	2	T36785	hypothetical prote
44	39	47.0	347	2	A81794	probable rotamase
45	39	47.0	348	2	B81216	peptidyl-prolyl ci

ALIGNMENTS

RESULT 1
G87332
hypothetical protein CC0674 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87332
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87332
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <STO>
A;Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:
C;Genetics:
A;Gene: CC0674

Query Match 57.8%; Score 48; DB 2; Length 389;
Best Local Similarity 64.7%; Pred. No. 3;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 APEKAKFEAFKAAAAPA 17
              | |   | ||||||||
Db         63 ADGKTSVETFKAAAAPA 79
```

RESULT 2
D83598
probable zinc proteinase PA0372 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83598
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <STO>
A;Cross-references: UNIPROT:Q9I6C2; GB:AE004475; GB:AE004091; NID:g9946221; PIDN:AAG037
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0372

Query Match 55.4%; Score 46; DB 2; Length 465;
Best Local Similarity 62.5%; Pred. No. 7.6;

```
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAPA 17
              |    || ||||| ||
Db        172 PNALAFERFKAAAYPA 187


RESULT 3
S77930
exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homar
A;Reference number: S77925
A;Accession: S77930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M496

  Query Match             54.8%;  Score 45.5;  DB 2;  Length 189;
  Best Local Similarity   66.7%;  Pred. No. 3.8;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 APEKAK-FEAFKAAAAPA 17
              | |||: |:||||| | |
Db          9 AAEKARFFQAFKAAEAAA 26


RESULT 4
S77935
exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77935
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homar
A;Reference number: S77925
A;Accession: S77935
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M495

  Query Match             54.8%;  Score 45.5;  DB 2;  Length 189;
  Best Local Similarity   66.7%;  Pred. No. 3.8;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 APEKAK-FEAFKAAAAPA 17
              | |||: |:||||| | |
Db          9 AAEKARFFQAFKAAEAAA 26


RESULT 5
F97683
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97683
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:g15157917; GSPDB:G
C;Genetics:
A;Gene: AGR_C_4900
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

  Query Match             54.2%;  Score 45;  DB 2;  Length 179;
  Best Local Similarity   64.7%;  Pred. No. 4.4;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              | |||: || | ||| |
Db        135 AEEKARLEAEKVAAAQA 151


RESULT 6
AF2908
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2908
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rplS
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

  Query Match             54.2%;  Score 45;  DB 2;  Length 179;
  Best Local Similarity   64.7%;  Pred. No. 4.4;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              | |||: || | ||| |
Db        135 AEEKARLEAEKVAAAQA 151


RESULT 7
G60110
repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: G60110
R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E
Infect. Immun. 57, 1959-1967, 1989
A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A;Reference number: A60110; MUID:89277508; PMID:2659529
A;Accession: G60110
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-97 <HOF>
A;Cross-references: UNIPROT:Q7M3W1
C;Superfamily: varicella-zoster virus gene 22 protein
C;Keywords: tandem repeat
F;1-85/Region: 7-residue repeats

  Query Match             53.0%;  Score 44;  DB 2;  Length 97;
  Best Local Similarity   64.7%;  Pred. No. 3.5;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
```

```
Db          2 APAKAAAAPAKAAAAPA 18


RESULT 8
AH3269
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) [imported] - Brucella melitensis (s
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3269
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3269
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <KUR>
A;Cross-references: UNIPROT:Q9L6H8; GB:AE008917; PIDN:AAL51323.1; PID:g17982020; GSPDB:G
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0141
A;Map position: I
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C;Keywords: acyltransferase; coenzyme A

  Query Match             53.0%;  Score 44;  DB 2;  Length 408;
  Best Local Similarity   64.7%;  Pred. No. 14;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || : | ||  ||||||
Db         86 APAQKKEEAKPAAAAPA 102


RESULT 9
T40464
probable RNA binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40464
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21931
A;Accession: T40464
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-128 <LYN>
A;Cross-references: UNIPROT:O94359; EMBL:AL034382; PIDN:CAA22287.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; cosmid c428
C;Genetics:
A;Gene: SPDB:SPBC428.12c
A;Map position: 2
A;Introns: 55/1; 108/1

  Query Match             51.8%;  Score 43;  DB 2;  Length 128;
  Best Local Similarity   46.7%;  Pred. No. 6.7;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAP 16
              || | |: ||: : |
Db        112 PESADFQTFKSTSTP 126


RESULT 10
T23177
hypothetical protein K01D12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23177; T23188
R;Dobson, R.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19703
A;Accession: T23177
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-84 <WIL>
A;Cross-references: UNIPROT:Q27223; UNIPROT:Q95QD3; EMBL:Z75543; PIDN:CAA99866.1; GSPDB
A;Experimental source: clone K01D12
A;Accession: T23188
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-84 <WI2>
A;Cross-references: EMBL:Z75543; PIDN:CAA99878.1; GSPDB:GN00023; CESP:K01D12.15
A;Experimental source: clone K01D12
C;Genetics:
A;Gene: CESP:K01D12.7; CESP:K01D12.15
A;Map position: 5

  Query Match             50.6%;  Score 42;  DB 2;  Length 84;
  Best Local Similarity   62.5%;  Pred. No. 6.5;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAPA 17
              | ||   | |||| ||
Db         34 PPKASASATKAAAPPA 49


RESULT 11
H70927
probable rpsP protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70927
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70927
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-162 <COL>
A;Cross-references: UNIPROT:Q10795; GB:Z74024; GB:AL123456; NID:g3250700; PIDN:CAA98346
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: rpsP

  Query Match             50.6%;  Score 42;  DB 2;  Length 162;
  Best Local Similarity   52.9%;  Pred. No. 12;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              ||: :| | | || | |
Db         97 APKPSKLEVFNAALAAA 113


RESULT 12
JV0057
tolA protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their prod
A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057
A;Molecule type: DNA
A;Residues: 1-421 <LEV>
A;Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g14801
A;Experimental source: strain JM105
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
```

```
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-421 <BLAT>
A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
C;Genetics:
A;Gene: tolA
A;Map position: 17 min
A;Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
F;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;355-362/Region: nucleotide-binding motif A (P-loop)

  Query Match             50.6%;  Score 42;  DB 2;  Length 421;
  Best Local Similarity   73.3%;  Pred. No. 31;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAA 15
              | |||| || | |||
Db        215 AAEKAKAEAEKKAAA 229


RESULT 13
F71062
hypothetical protein PH1196 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: F71062
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71062
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-743 <KAW>
A;Cross-references: UNIPROT:O58900; GB:AP000005; NID:g3236132; PIDN:BAA30296.1; PID:g325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1196

  Query Match             50.6%;  Score 42;  DB 2;  Length 743;
  Best Local Similarity   52.9%;  Pred. No. 55;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              ||| ||| ||:   : |
Db        388 APEAAKFTAPQTKVSGA 404


RESULT 14
AH2752
dihydrolipoamide acetyltransferase [imported] - Agrobacterium tumefaciens (strain C58, D
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2752
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2752
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <KUR>
A;Cross-references: UNIPROT:Q8UFG5; GB:AE008688; PIDN:AAL42438.1; PID:g17739851; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: aceF
A;Map position: circular chromosome

  Query Match             49.4%;  Score 41;  DB 2;  Length 405;
  Best Local Similarity   66.7%;  Pred. No. 44;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAP 16
              || || || |  |||
Db         56 PEAAKAEAPKEEAAP 70


RESULT 15
AB3359
dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) [imported] - Brucella melitensis (str
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3359
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <KUR>
A;Cross-references: UNIPROT:Q8YHE5; GB:AE008917; PIDN:AAL52037.1; PID:g17982803; GSPDB:G
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0856
A;Map position: I
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C;Keywords: acyltransferase; coenzyme A

  Query Match             49.4%;  Score 41;  DB 2;  Length 447;
  Best Local Similarity   62.5%;  Pred. No. 49;
  Matches   10;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAPA 17
              | :|| ||   |||||
Db        106 PAEAKKEAAAPAAAPA 121


Search completed: April  4, 2005, 17:27:07
Job time : 30.1562 secs
```

OM protein - protein search, using sw model

Run on: April 4, 2005, 17:02:08 ; Search time 125.906 Seconds
(without alignments)
69.141 Million cell updates/sec

Title: US-10-056-583A-96
Perfect score: 83
Sequence: 1 APEKAKPEAFKAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	60.2	574	2	Q8SXM8	Q8sxm8 drosophila
2	50	60.2	607	2	Q9W327	Q9w327 drosophila
3	48	57.8	389	2	Q9AAC8	Q9aac8 caulobacter
4	46	55.4	465	2	Q9I6C2	Q9i6c2 pseudomonas
5	45.5	54.8	189	2	Q7M495	Q7m495 homarus ame
6	45.5	54.8	189	2	Q7M496	Q7m496 homarus ame
7	45	54.2	179	1	RL19_AGRT5	Q8ubz5 agrobacteri
8	45	54.2	183	2	Q81W24	Q81w24 bacillus an
9	45	54.2	607	2	Q8PGF8	Q8pgf8 xanthomonas
10	45	54.2	836	2	Q8PSL8	Q8psl8 methanosarc
11	44	53.0	97	2	Q7M3W1	Q7m3w1 trypanosoma
12	44	53.0	353	2	Q87HZ8	Q87hz8 vibrio para
13	44	53.0	390	2	O85598	O85598 brucella ab
14	44	53.0	408	2	Q8FYF8	Q8fyf8 brucella su
15	44	53.0	408	2	Q9L6H8	Q9l6h8 brucella me
16	44	53.0	593	2	Q6AQK4	Q6aqk4 desulfotale
17	43.5	52.4	306	2	Q7XJ35	Q7xj35 medicago tr
18	43	51.8	116	2	O94359	O94359 schizosacch
19	43	51.8	151	2	Q95Z67	Q95z67 ostertagia
20	43	51.8	174	2	Q73FJ2	Q73fj2 bacillus ce
21	43	51.8	250	2	Q7NW09	Q7nw09 chromobacte
22	43	51.8	677	2	Q62E59	Q62e59 burkholderi
23	43	51.8	677	2	Q63J18	Q63j18 burkholderi
24	42.5	51.2	300	2	Q729M4	Q729m4 desulfovibr
25	42	50.6	87	2	Q8TJG9	Q8tjg9 methanosarc
26	42	50.6	162	1	RS16_MYCBO	P66436 mycobacteri
27	42	50.6	162	1	RS16_MYCTU	P66435 mycobacteri
28	42	50.6	177	1	RL19_RHIME	Q92I39 rhizobium m
29	42	50.6	181	1	RL19_RHILO	P58168 rhizobium l
30	42	50.6	273	2	Q72CN6	Q72cn6 desulfovibr
31	42	50.6	413	2	Q83SA1	Q83sa1 shigella fl
32	42	50.6	421	1	TOLA_ECOLI	P19934 escherichia
33	42	50.6	421	2	Q8FJT1	Q8fjt1 escherichia
34	42	50.6	570	2	Q96M46	Q96m46 homo sapien
35	42	50.6	707	2	Q64CP3	Q64cp3 uncultured
36	42	50.6	743	2	O58900	O58900 pyrococcus
37	41.5	50.0	307	2	Q9M523	Q9m523 tsuga heter
38	41.5	50.0	307	2	Q9M524	Q9m524 tsuga heter
39	41.5	50.0	458	2	Q7SDS7	Q7sds7 neurospora
40	41.5	50.0	629	2	Q8XNK8	Q8xnk8 clostridium
41	41	49.4	114	2	O85393	O85393 coxiella bu
42	41	49.4	145	2	Q7Y3M5	Q7y3m5 enterobacte
43	41	49.4	183	2	Q63HF5	Q63hf5 bacillus ce
44	41	49.4	183	2	Q6HPZ7	Q6hpz7 bacillus th
45	41	49.4	240	2	Q83BL1	Q83bl1 coxiella bu

ALIGNMENTS

RESULT 1
Q8SXM8
ID Q8SXM8 PRELIMINARY; PRT; 574 AA.
AC Q8SXM8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LD23509p (CG12141-PA).
GN Name=Aats-lys; ORFNames=CG12141;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

```
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
DR   EMBL; AY089547; AAL90285.1; -.
DR   EMBL; AE003447; AAN09255.1; -.
DR   HSSP; P13030; 1BBW.
DR   FlyBase; FBgn0027084; Aats-lys.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0004815; F:aspartate-tRNA ligase activity; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016874; F:ligase activity; IEA.
DR   GO; GO:0004824; F:lysine-tRNA ligase activity; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0006422; P:aspartyl-tRNA aminoacylation; IEA.
DR   GO; GO:0006430; P:lysyl-tRNA aminoacylation; IEA.
DR   GO; GO:0006412; P:protein biosynthesis; IEA.
DR   InterPro; IPR008994; Nucleic_acid_OB.
DR   InterPro; IPR004364; tRNA-synt_2.
DR   InterPro; IPR002312; tRNA-synt_asp.
DR   InterPro; IPR002313; tRNA-synt_lys_2.
DR   InterPro; IPR004365; tRNA_anti.
DR   InterPro; IPR006195; tRNA_ligase_II.
DR   Pfam; PF00152; tRNA-synt_2; 1.
DR   Pfam; PF01336; tRNA_anti; 1.
DR   PRINTS; PR01042; TRNASYNTHASP.
DR   PRINTS; PR00982; TRNASYNTHLYS.
DR   TIGRFAMs; TIGR00499; lysS_bact; 1.
DR   PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW   ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
SQ   SEQUENCE   574 AA;  64660 MW;  861DAEA9C53E0DBE CRC64;

  Query Match             60.2%;  Score 50;  DB 2;  Length 574;
  Best Local Similarity   70.6%;  Pred. No. 11;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              | :||| :| |||||||
Db         19 AEQKAKEKAEKAAAAPA 35


RESULT 2
Q9W327
ID   Q9W327      PRELIMINARY;      PRT;   607 AA.
AC   Q9W327;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG12141-PB.
GN   ORFNames=CG12141;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
```

```
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
DR   EMBL; AE003447; AAF46510.2; -.
DR   HSSP; P13030; 1BBW.
DR   FlyBase; FBgn0027084; Aats-lys.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0004815; F:aspartate-tRNA ligase activity; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016874; F:ligase activity; IEA.
DR   GO; GO:0004824; F:lysine-tRNA ligase activity; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0006422; P:aspartyl-tRNA aminoacylation; IEA.
DR   GO; GO:0006430; P:lysyl-tRNA aminoacylation; IEA.
DR   GO; GO:0006412; P:protein biosynthesis; IEA.
DR   InterPro; IPR008994; Nucleic_acid_OB.
DR   InterPro; IPR004364; tRNA-synt_2.
DR   InterPro; IPR002312; tRNA-synt_asp.
DR   InterPro; IPR002313; tRNA-synt_lys_2.
DR   InterPro; IPR004365; tRNA_anti.
DR   InterPro; IPR006195; tRNA_ligase_II.
DR   Pfam; PF00152; tRNA-synt_2; 1.
DR   Pfam; PF01336; tRNA_anti; 1.
DR   PRINTS; PR01042; TRNASYNTHASP.
DR   PRINTS; PR00982; TRNASYNTHLYS.
DR   TIGRFAMs; TIGR00499; lysS_bact; 1.
DR   PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW   ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
SQ   SEQUENCE   607 AA;  68503 MW;  771CE9870963D81B CRC64;

  Query Match            60.2%;  Score 50;  DB 2;  Length 607;
  Best Local Similarity  70.6%;  Pred. No. 11;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              | :||| :| |||||||
Db         52 AEQKAKEKAEKAAAAPA 68


RESULT 3
Q9AAC8
ID   Q9AAC8      PRELIMINARY;      PRT;   389 AA.
AC   Q9AAC8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein CC0674.
GN   OrderedLocusNames=CC0674;
OS   Caulobacter crescentus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC   Caulobacteraceae; Caulobacter.
OX   NCBI_TaxID=155892;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA   Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA   Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA   Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA   Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA   Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA   Fraser C.M.;
RT   "Complete genome sequence of Caulobacter crescentus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR   EMBL; AE005743; AAK22659.1; -.
DR   PIR; G87332; G87332.
DR   TIGR; CC0674; -.
DR   InterPro; IPR008262; Lipase_AS.
DR   InterPro; IPR000897; SRP54.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR   PROSITE; PS00300; SRP54; UNKNOWN_1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   389 AA;  40769 MW;  C6DD05B8CE8D150E CRC64;

  Query Match            57.8%;  Score 48;  DB 2;  Length 389;
  Best Local Similarity  64.7%;  Pred. No. 16;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              |  |   | ||||||||
Db         63 ADGKTSVETFKAAAAPA 79


RESULT 4
Q9I6C2
ID   Q9I6C2      PRELIMINARY;      PRT;   465 AA.
AC   Q9I6C2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Probable zinc protease.
GN   OrderedLocusNames=PA0372;
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
```

```
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004475; AAG03761.1; -.
DR   PIR; D83598; D83598.
DR   GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001431; Insulinase_like.
DR   InterPro; IPR007863; Peptidase_M16_C.
DR   Pfam; PF00675; Peptidase_M16; 1.
DR   Pfam; PF05193; Peptidase_M16_C; 1.
KW   Complete proteome; Protease.
SQ   SEQUENCE   465 AA;  51975 MW;  8D20E91407605A91 CRC64;

  Query Match             55.4%;  Score 46;  DB 2;  Length 465;
  Best Local Similarity   62.5%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 PEKAKFEAFKAAAAPA 17
              |    || ||||| ||
Db        172 PNALAFERFKAAAYPA 187


RESULT 5
Q7M495
ID   Q7M495      PRELIMINARY;      PRT;   189 AA.
AC   Q7M495;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Exoskeletal protein HACP202B (Fragment).
OS   Homarus americanus (American lobster).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC   Nephropoidea; Nephropidae; Homarus.
OX   NCBI_TaxID=6706;
RN   [1]
RP   SEQUENCE.
RA   Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL   Submitted (JUN-1997) to the PIR data bank.
DR   PIR; S77935; S77935.
FT   NON_TER       1      1
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  20180 MW;  72A4EFCD9C7ECFE9 CRC64;

  Query Match             54.8%;  Score 45.5;  DB 2;  Length 189;
  Best Local Similarity   66.7%;  Pred. No. 20;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 APEKAK-FEAFKAAAAPA 17
              | |||: |:||||| | |
Db          9 AAEKARFFQAFKAAEAAA 26


RESULT 6
Q7M496
ID   Q7M496      PRELIMINARY;      PRT;   189 AA.
AC   Q7M496;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Exoskeletal protein HACP202A (Fragment).
OS   Homarus americanus (American lobster).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC   Nephropoidea; Nephropidae; Homarus.
OX   NCBI_TaxID=6706;
RN   [1]
RP   SEQUENCE.
RA   Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL   Submitted (JUN-1997) to the PIR data bank.
DR   PIR; S77930; S77930.
FT   NON_TER       1      1
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  20154 MW;  72A4EFCD9C647FE9 CRC64;

  Query Match             54.8%;  Score 45.5;  DB 2;  Length 189;
  Best Local Similarity   66.7%;  Pred. No. 20;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 APEKAK-FEAFKAAAAPA 17
              | |||: |:||||| | |
Db          9 AAEKARFFQAFKAAEAAA 26


RESULT 7
RL19_AGRT5
ID   RL19_AGRT5     STANDARD;      PRT;   179 AA.
AC   Q8UBZ5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   50S ribosomal protein L19.
GN   Name=rplS; OrderedLocusNames=Atu2703, AGR_C_4900;
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
CC   -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC       interface and may play a role in the structure and function of the
CC       aminoacyl-tRNA binding site (By similarity).
CC   -!- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE009216; AAL43684.1; -.
DR   EMBL; AE008183; AAK88423.1; -.
DR   PIR; AF2908; AF2908.
DR   PIR; F97683; F97683.
```

```
DR   HAMAP; MF_00402; -; 1.
DR   InterPro; IPR001857; Ribosomal_L19.
DR   Pfam; PF01245; Ribosomal_L19; 1.
DR   PRINTS; PR00061; RIBOSOMALL19.
DR   ProDom; PD002979; Ribosomal_L19; 1.
DR   TIGRFAMs; TIGR01024; rplS_bact; 1.
DR   PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW   Complete proteome; Ribosomal protein.
SQ   SEQUENCE   179 AA;  19474 MW;  F3256BA44A5AD2D1 CRC64;

  Query Match             54.2%;  Score 45;  DB 1;  Length 179;
  Best Local Similarity   64.7%;  Pred. No. 23;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              | |||: || | ||| |
Db        135 AEEKARLEAEKVAAAQA 151


RESULT 8
Q81W24
ID   Q81W24      PRELIMINARY;      PRT;   183 AA.
AC   Q81W24; Q6I526; Q6KYS0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BA0013, BAS0016, GBAA0013;
OS   Bacillus anthracis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1392;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ames / isolate Porton;
RX   MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA   Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA   Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA   Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA   Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA   DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA   Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA   Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA   Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA   Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA   Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA   Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT   "The genome sequence of Bacillus anthracis Ames and comparison to
RT   closely related bacteria.";
RL   Nature 423:81-86(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ames / isolate 0581;
RA   Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA   Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA   Fraser C.M.;
RT   "Bacillus anthracis comparative genomics.";
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sterne;
RA   Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA   Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA   Richardson P., Rubin E., Tice H.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE017024; AAP24070.1; -.
DR   EMBL; AE017334; AAT29093.1; -.
DR   EMBL; AE017225; AAT52355.1; -.
DR   TIGR; BA0013; -.
DR   TIGR; GBAA0013; -.
DR   InterPro; IPR009058; Wing_hlx_DNA_bnd.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   183 AA;  20653 MW;  3BD4AC2C8D658752 CRC64;

  Query Match             54.2%;  Score 45;  DB 2;  Length 183;
  Best Local Similarity   62.5%;  Pred. No. 24;
  Matches   10;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAP 16
              ||:| | || |  |||
Db        116 APKKVKKEAVKKEAAP 131


RESULT 9
Q8PGF8
ID   Q8PGF8      PRELIMINARY;      PRT;   607 AA.
AC   Q8PGF8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Dihydrolipoamide dehydrogenase.
GN   Name=lpdA; OrderedLocusNames=XAC3659;
OS   Xanthomonas axonopodis (pv. citri).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xanthomonas.
OX   NCBI_TaxID=92829;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=306 / ATCC 13902 / XV 101;
RX   MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA   da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA   Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA   Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA   Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA   Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA   Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA   Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA   Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA   Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA   Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA   Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA   Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA   Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA   Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA   Setubal J.C., Kitajima J.P.;
RT   "Comparison of the genomes of two Xanthomonas pathogens with differing
RT   host specificities.";
RL   Nature 417:459-463(2002).
CC   -!- CATALYTIC ACTIVITY: Protein N(6)-(dihydrolipoyl)lysine + NAD(+) =
CC       protein N(6)-(lipoyl)lysine + NADH.
CC   -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC   -!- COFACTOR: FAD (By similarity).
CC   -!- MISCELLANEOUS: The active site is a redox-active disulfide bond
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
CC       oxidoreductase family.
CC   -!- SIMILARITY: Contains 1 lipoyl-binding domain.
DR   EMBL; AE012016; AAM38502.1; -.
DR   HSSP; Q51225; 1OJT.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0004148; F:dihydrolipoyl dehydrogenase activity; IEA.
DR   GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0006096; P:glycolysis; IEA.
DR   InterPro; IPR000089; Biotin_lipoyl.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR000815; Hg_reductase.
DR   InterPro; IPR011053; Hybrid_motif.
DR   InterPro; IPR006258; Lipoamide_dh.
DR   InterPro; IPR003016; Lipoyl_BS.
DR   InterPro; IPR000205; NAD_BS.
DR   InterPro; IPR001100; Pyr_redox.
DR   InterPro; IPR004099; Pyr_redox_dim.
DR   Pfam; PF00364; Biotin_lipoyl; 1.
DR   Pfam; PF00070; Pyr_redox; 1.
DR   Pfam; PF02852; Pyr_redox_dim; 1.
```

```
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00945; HGRDTASE.
DR   PRINTS; PR00411; PNDRDTASEI.
DR   ProDom; PD000139; FAD_pyr_redox; 1.
DR   TIGRFAMs; TIGR01350; lipoamide_DH; 1.
DR   PROSITE; PS00189; LIPOYL; 1.
DR   PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
KW   Complete proteome; FAD; Flavoprotein; Lipoyl; NAD; Oxidoreductase;
KW   Redox-active center.
SQ   SEQUENCE   607 AA;  63213 MW;  2D218BCF97903D9F CRC64;

  Query Match             54.2%;  Score 45;  DB 2;  Length 607;
  Best Local Similarity   64.7%;  Pred. No. 75;
  Matches   11;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||: :|  ||||||
Db         84 APAKAEPKAAPAAAAPA 100


RESULT 10
Q8PSL8
ID   Q8PSL8      PRELIMINARY;      PRT;   836 AA.
AC   Q8PSL8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein MM3061.
GN   OrderedLocusNames=MM3061;
OS   Methanosarcina mazei (Methanosarcina frisia).
OC   Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2209;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Goe1 / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX   MEDLINE=22120827; PubMed=12125824;
RA   Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA   Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
RA   Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA   Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA   Fritz H.-J., Gottschalk G.;
RT   "The genome of Methanosarcina mazei: evidence for lateral gene
RT   transfer between Bacteria and Archaea.";
RL   J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR   EMBL; AE013561; AAM32757.1; -.
KW   Complete proteome.
SQ   SEQUENCE   836 AA;  93347 MW;  DFCE3FF75DD0153B CRC64;

  Query Match             54.2%;  Score 45;  DB 2;  Length 836;
  Best Local Similarity   60.0%;  Pred. No. 1e+02;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAA 15
              |||| | | |:| |:
Db        819 APEKGKIEIFEAIAS 833


RESULT 11
Q7M3W1
ID   Q7M3W1      PRELIMINARY;      PRT;    97 AA.
AC   Q7M3W1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Repetitive protein antigen 69/70 (Fragment).
OS   Trypanosoma cruzi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX   NCBI_TaxID=5693;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89277508; PubMed=2659529;
RA   Hoft D.F., Kim K.S., Otsu K., Moser D.R., Yost W.J., Blumin J.H.,
RA   Donelson J.E., Kirchhoff L.V.;
RT   "Trypanosoma cruzi expresses diverse repetitive protein antigens.";
RL   Infect. Immun. 57:1959-1967(1989).
DR   PIR; G60110; G60110.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0005840; C:ribosome; IEA.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR   GO; GO:0006412; P:protein biosynthesis; IEA.
DR   InterPro; IPR001859; Ribosomal_P2.
DR   PRINTS; PR00456; RIBOSOMALP2.
FT   NON_TER       1      1
FT   NON_TER      97     97
SQ   SEQUENCE   97 AA;  8210 MW;  477B46BEE0DFE3E2 CRC64;

  Query Match             53.0%;  Score 44;  DB 2;  Length 97;
  Best Local Similarity   64.7%;  Pred. No. 19;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || ||     |||||||
Db          2 APAKAAAAPAKAAAAPA 18


RESULT 12
Q87HZ8
ID   Q87HZ8      PRELIMINARY;      PRT;   353 AA.
AC   Q87HZ8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative periplasmic linker protein.
GN   OrderedLocusNames=VPA0808;
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RIMD 2210633 / Serotype O3:K6;
RX   MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT   distinct from that of V. cholerae.";
RL   Lancet 361:743-749(2003).
DR   EMBL; AP005086; BAC62151.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0015428; F:type I protein secretor activity; IEA.
DR   GO; GO:0009306; P:protein secretion; IEA.
DR   InterPro; IPR006143; HlyD.
DR   InterPro; IPR003997; RtxD.
DR   InterPro; IPR011054; Rudmnt_hyb_motif.
DR   PRINTS; PR01490; RTXTOXIND.
DR   TIGRFAMs; TIGR01730; RND_mfp; 1.
KW   Complete proteome.
SQ   SEQUENCE   353 AA;  38932 MW;  BBB222D4212CE833 CRC64;

  Query Match             53.0%;  Score 44;  DB 2;  Length 353;
  Best Local Similarity   47.1%;  Pred. No. 66;
  Matches    8;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || |::: |||    ||
Db         40 APVKSQYRAFKGLVVPA 56


RESULT 13
O85598
ID   O85598      PRELIMINARY;      PRT;   390 AA.
AC   O85598;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
```

```
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Dihydrolipoamide succinyl transferase.
OS   Brucella abortus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=235;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S19;
RA   Boschiroli L., Cravero S., Rosetti O.L.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
DR   EMBL; AF070932; AAC23605.1; -.
DR   HSSP; P07016; 1C4T.
DR   GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR   InterPro; IPR001078; 2Oxoacid_dh.
DR   InterPro; IPR000089; Biotin_lipoyl.
DR   InterPro; IPR004167; E3_binding.
DR   InterPro; IPR011053; Hybrid_motif.
DR   InterPro; IPR006255; SucB.
DR   Pfam; PF00198; 2-oxoacid_dh; 1.
DR   Pfam; PF00364; Biotin_lipoyl; 1.
DR   Pfam; PF02817; E3_binding; 1.
DR   ProDom; PD001115; 2Oxoacid_dh; 1.
DR   TIGRFAMs; TIGR01347; sucB; 1.
KW   Acyltransferase; Lipoyl; Transferase.
SQ   SEQUENCE   390 AA;  41004 MW;  5A0AADE87569F5C2 CRC64;

  Query Match             53.0%;  Score 44;  DB 2;  Length 390;
  Best Local Similarity   64.7%;  Pred. No. 72;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || : | ||  ||||||
Db         71 APAQKKEEAKPAAAAPA 87


RESULT 14
Q8FYF8
ID   Q8FYF8      PRELIMINARY;      PRT;   408 AA.
AC   Q8FYF8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide
DE   succinyltransferase (EC 2.3.1.61).
GN   Name=sucB; OrderedLocusNames=BR1922;
OS   Brucella suis.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=29461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1330 / Biovar 1;
RX   MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA   Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA   Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA   Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA   Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA   Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA   Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA   Fraser C.M.;
RT   "The Brucella suis genome reveals fundamental similarities between
RT   animal and plant pathogens and symbionts.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC   -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC   -!- SIMILARITY: Contains 1 lipoyl-binding domain.
DR   EMBL; AE014482; AAN30814.1; -.
DR   HSSP; P07016; 1C4T.
DR   TIGR; BR1922; -.
DR   GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR   InterPro; IPR001078; 2Oxoacid_dh.
DR   InterPro; IPR000089; Biotin_lipoyl.
DR   InterPro; IPR004167; E3_binding.
DR   InterPro; IPR011053; Hybrid_motif.
DR   InterPro; IPR003016; Lipoyl_BS.
DR   InterPro; IPR006255; SucB.
DR   Pfam; PF00198; 2-oxoacid_dh; 1.
DR   Pfam; PF00364; Biotin_lipoyl; 1.
DR   Pfam; PF02817; E3_binding; 1.
DR   ProDom; PD001115; 2Oxoacid_dh; 1.
DR   TIGRFAMs; TIGR01347; sucB; 1.
DR   PROSITE; PS00189; LIPOYL; 1.
KW   Acyltransferase; Complete proteome; Lipoyl; Transferase.
SQ   SEQUENCE   408 AA;  42839 MW;  7EC80A61800ACC64 CRC64;

  Query Match             53.0%;  Score 44;  DB 2;  Length 408;
  Best Local Similarity   64.7%;  Pred. No. 75;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || : | ||  ||||||
Db         86 APAQKKEEAKPAAAAPA 102


RESULT 15
Q9L6H8
ID   Q9L6H8      PRELIMINARY;      PRT;   408 AA.
AC   Q9L6H8; Q7CNV5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE
DE   DEHYDROGENASE COMPLEX (EC 2.3.1.61).
GN   Name=sucB; OrderedLocusNames=BMEI0141;
OS   Brucella melitensis.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=29459;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16M;
RX   MEDLINE=21437665; PubMed=11553602;
RX   DOI=10.1128/IAI.69.10.6537-6540.2001;
RA   Zygmunt M.S., Diaz M.A., Teixeira-Gomes A.P., Cloeckaert A.;
RT   "Cloning, nucleotide sequence, and expression of the Brucella
RT   melitensis sucB gene coding for an immunogenic dihydrolipoamide
RT   succinyltransferase homologous protein.";
RL   Infect. Immun. 69:6537-6540(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16M / ATCC 23456 / Biotype 1;
RX   MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
RA   DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA   Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA   Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA   Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA   Haselkorn R., Kyrpides N.C., Overbeek R.;
RT   "The genome sequence of the facultative intracellular pathogen
RT   Brucella melitensis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC   -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC   -!- SIMILARITY: Contains 1 lipoyl-binding domain.
DR   EMBL; AF235020; AAF43701.1; -.
DR   EMBL; AE009457; AAL51323.1; -.
```

```
DR   PIR; AH3269; AH3269.
DR   HSSP; P07016; 1C4T.
DR   GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR   InterPro; IPR001078; 2Oxoacid_dh.
DR   InterPro; IPR000089; Biotin_lipoyl.
DR   InterPro; IPR004167; E3_binding.
DR   InterPro; IPR011053; Hybrid_motif.
DR   InterPro; IPR003016; Lipoyl_BS.
DR   InterPro; IPR006255; SucB.
DR   Pfam; PF00198; 2-oxoacid_dh; 1.
DR   Pfam; PF00364; Biotin_lipoyl; 1.
DR   Pfam; PF02817; E3_binding; 1.
DR   ProDom; PD001115; 2Oxoacid_dh; 1.
DR   TIGRFAMs; TIGR01347; sucB; 1.
DR   PROSITE; PS00189; LIPOYL; 1.
KW   Acyltransferase; Complete proteome; Lipoyl; Transferase.
SQ   SEQUENCE   408 AA;  42911 MW;  16E763942B097CA7 CRC64;

  Query Match             53.0%;  Score 44;  DB 2;  Length 408;
  Best Local Similarity   64.7%;  Pred. No. 75;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APEKAKFEAFKAAAAPA 17
              || : | ||  ||||||
Db         86 APAQKKEEAKPAAAAPA 102


Search completed: April  4, 2005, 17:31:10
Job time : 128.906 secs
```